Testing Species Boundaries in the Staphylinid Beetle Genus *Mocyta* (Insecta, Coleoptera, Staphylinidae)

Master of Science in Ecology and Evolution

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Natural History Museum
University of Oslo
2014

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http://www.duo.uio.no
Trykk: Reprosentralen, Universitetet i Oslo

Acknowledgements

This work was in part supported by SIU grant HNP-2012/10118 to Vladimir Gusarov. Thank you, Vladimir Gusarov for giving me this opportunity and for introducing me to the interesting world of athetine beetles. Your bottomless knowledge and sense of humour is highly esteemed. Lutz Bachmann, thank you for helping me with the molecular work, for the tips and tricks regarding my thesis and for making me laugh.

Thank you, Hallvard Elven for suggestions and interesting conversations. Maria Mavrikidi, thank you for re-extracting and re-sequencing the 'troublesome' specimens. To all at the DNA lab at NHM, your assistance and company is invaluable. Special thanks go to Judith Osswald for introducing me to the lab, Eve Zeyl and Virginia Mirre for technical support, and lab manager Audun Schrøder-Nielsen for always having time to spare.

Nikolai Yunakov and Peter Hammond, the specimens you provided for this study are highly appreciated. To Renee Labbee and Jeremy DeWaard at the Biodiversity Institute of Ontario, Mikko Pentinsaari at the University of Oulu, Oscar Vorst at Biodiversity Centre in Leiden and Jérôme Morinière at GBOL, thank you all for providing CO1 sequences from *Mocyta* specimens for my initial analyses, and thank you James Robertson at Bold for the referrals. I would also like to express my gratitude to Lars Jermiin, Henrik Enghoff, Boy Overgaard Nielsen, Jan Pedersen, Frank Jensen and Alexey Solodovnikov for trying to locate a copy of Viggo Mahler's thesis "*Acrotona* studies".

Trude Magnussen and Kristine Dobbe, thank you for your support, company and long coffee breaks. To all at NHM, thank you for being so welcoming!

June Susanne Berg, my dearest friend, thank you for your patience and discussions regarding this thesis. My beloved mother, you are an endless source of support and encouragement. Erik, no words can express my gratitude, without you, this thesis would never have existed.

Eilen B. Josefsen

Oslo, 4th of August 2014

Abstract

The taxonomy of the staphylinid genus *Mocyta* was explored using molecular markers, in addition to a thorough investigation of the published literature regarding this genus and its proposed morphospecies. The aim was to test if the recognized morphospecies differ genetically, and if popular species delimitation methods can be used to delineate these species. Furthermore, the most widespread and also most common species in Norway, *Mocyta fungi*, was examined in more detail to test if any geographic patterns are reflected in the genetic variation, and if this variation correlates with ecological preferences. This study also aimed to explore if the parthenogenetic populations of *M. fungi* are restricted geographically.

In total, 111 *Mocyta* specimens, representing 12 morphospecies from 17 countries, were included in the analyses. Both maximum likelihood and Bayesian inference were employed on two PCR amplified molecular markers (the mitochondrial cytochrome oxidase subunit 1 and the internal transcribed spacer 2 of the nuclear ribosomal gene cluster) to investigate the phylogenetic relationship of these morphospecies. In addition, calculations of mean intra- and interspecific genetic distances were used to delimit species. Online service for delimiting species using Bayesian implementation of the PTP model (bPTP) was also applied. Haplotype networks were used to investigate the genetic variation among specimens of *M. fungi*.

The maximum likelihood and Bayesian inference analyses grouped the morphospecies together in well-supported clades, but the species delimitation methods applied failed to confirm this. The bPTP method estimated many species, exceeding the number of morphospecies, but the supports for these were generally low. There were no evident geographic patterns reflected in the genetic variation of *M. fungi*, nor any correlation between genetic variation and ecological preferences. Biased representation of specimens from different countries made it impossible to confidently compare the genetic variation between specimens from Norwegian populations and specimens from populations elsewhere. Even though all 33 specimens of *M. fungi* were females, the parthenogenetic populations of *M. fungi* could not be examined outside Norway because too few non-Norwegian specimens were included.

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Introduction

Coleoptera (beetles) are the largest order of insects, estimated to comprise about 500,000 species worldwide. The key characteristic of beetles is their thick and sclerotized anterior pair of wings (elytra) which function as wing cases, protecting the underlying membranous posterior wings. Staphylinidae (rove beetles) are a family of beetles that are primarily identified by their short elytra leaving their abdomen exposed. Rove beetles are considered the largest beetle family, consisting of more than 52,500 species spanning over thousands of genera worldwide (Thayer 2005; Grebennikov & Newton 2009).

Subfamily Aleocharinae Fleming, 1821

Aleocharinae comprise more than 1,000 genera and almost 13,000 described species worldwide, making it the largest subfamily of staphylinid beetles (Thayer 2005). The subfamily is represented on all continents except Antarctica, and 610 species have been recorded in Norway (Artsdatabanken 2014a).

Based on a unique synapomorphy (lateral lobes of the aedeagus, or parameres, large) Aleocharinae were first proven to be monophyletic in 1975 (Hammond 1975). The monophyly was later supported by two larval synapomorphies (Ashe & Newton 1993). The subfamily is divided into two groups, the 'basal' and 'higher' Aleocharinae (Ashe & Newton 1993), and the 'higher' Aleocharinae are well supported as a monophyletic group in recent molecular research (Osswald *et al.* 2013).

Tribe Athetini Casey, 1910

The tribe Athetini (Artsdatabanken 2014b) includes thousands of species in 173 genera worldwide (Newton *et al.* 2000), and more than half (310) of all the species of Aleocharinae registered in Norway belong to this tribe. All species within the tribe are small beetles, with a body just a few millimetres long. For most parts of the world there are no comprehensive modern revisions of the tribe. The most recent world generic revision is by Fenyes from 1918-21. This makes identification of species in this tribe difficult. In Central and Northern Europe the situation is somewhat better as more recent keys to genera and species are available (e.g. Brundin 1952; Palm 1970; Benick & Lohse 1974).

Genus *Mocyta* Mulsant & Rey, 1874

Diagnosis*:* The body is dark and has a fusiform shape, with short side bristles. The infraorbital carina is complete. The pronotum is glossy with pubescence at the midline directed backwards, while at the sides it is directed obliquely backwards and outwards. The pronotum is widest at the middle, and more narrowing anteriorly than posteriorly. The hypomeron is not visible in lateral view, due to the arched shape of the pronotum. The 7th tergite has a transverse wavy microsculpture with cells approximately twice as wide as long. The punctation on the abdomen becomes less pronounced towards the apex. The bristle on mesotibia is delicate, yet well-defined, and rarely longer than the diameter of the tibia. The bristle on metatibia is short and inconspicuous. The metatarsi are slender and significantly shorter than the tibiae, and the 1st segment is never longer than the 2nd. The tarsal claw is approximately 1/3 (or longer) than the length of the tarsus (Brundin 1952; Palm 1970; Benick & Lohse 1974; Lohse *et al.* 1990).

Systematics: The genus *Mocyta* was first proposed by Mulsant and Rey (1874, Planche II) as a subgenus of *Colpodota* Mulsant & Rey, 1873, and *Aleochara fungi* (Gravenhorst, 1806) was subsequently designated as type species by Blackwelder (1952, p. 250). There were nine species originally included in this subgenus, of which only five are still considered *Mocyta* species. Blackwelder (1952, p. 250) claims that the name *Mocyta* was "inadvertently used as a subgenus of *Colpodota*" in the plate, because in the text all the species of this subgenus "were placed under the subgenus Acrotona". The subgenus *Acrotona* Thomson, 1859 of *Colpodota* included many of the species now regarded as members of *Mocyta*. Ganglbauer (1895) moved the subgenus *Acrotona* to the large genus *Atheta* Thomson, 1858, and it was Benick and Lohse (1974) who first listed *Mocyta* as a subgenus of *Atheta.* Lohse *et al.* (1990) regarded *Mocyta* as a separate genus in their revision of North American arctic aleocharines. In the yet most comprehensive phylogenetic analysis of the tribe Athetini, the two included species of *Mocyta* formed a well-supported clade together with the *Atheta* subgenera *Mycetota* Ádám, 1987 and *Oxypodera* Bernhauer, 1915 in the tribe Athetini (Elven *et al.* 2010). However, there is a need of a thorough revision of the genus *Mocyta* and study of its relationship to other genera (Brundin 1952; Mahler 1988; Newton *et al.* 2000; Assing & Schülke 2006).

Species identification: Identification of species belonging to *Mocyta* is difficult and various authors list different sets of species in the genus (e.g. Silfverberg (2004): seven species; Löbl and Smetana (2004) list *Mocyta* as synonym of the genus *Acrotona*: 125 species; Mulsant and Rey (1873, Planche II) and Benick and Lohse (1974): nine species; and Brundin (1952) and Palm (1970) as "die *fungi*-Gruppe" in *Atheta* (*Acrotona*): five species). In most staphylinids genitalic characters are very useful for species identification, but in *Mocyta* there seems to be only few or no reliable characters (Brundin 1952). However, Lohse *et al.* (1990) proposed that the absolute length of the spermatheca may be suitable for species identification. In parthenogenetic species, though, there is little or no selection pressure on genital morphology due to the lack of males. Consequently, the shape of the female genitalia can vary freely and may become an unreliable character for identification (Jermiin & Mahler 1993). Given that the most widespread species of *Mocyta*, *M. fungi* (Gravenhorst, 1806), seems to be parthenogenetic (Topp 1974; Topp 1975; Lohse & Smetana 1985; Lohse *et al.* 1990), and shows great variation in genital morphology (Strand & Vik 1964; Benick & Lohse 1974; Topp 1974), other methods should be used to confirm species identification.

Species Concepts

To be able to delimit species it is necessary to refer to specific species concepts. There are many concepts to choose from and biologist employ various definitions depending on their field of specialisation (Cracraft 1989; Mayden 1997; Hausdorf 2011). Accumulative information about speciation processes and the 'organization' of uniparental organisms has revived the search for a general species concept (Hausdorf 2011). The phylogenetic species concept defines a species as the smallest set of individuals that share a unique combination of character states (Wheeler & Platnick 2000). This concept can be employed both for morphological characters, molecular data or a combination of both (Wheeler & Platnick 2000). In this study this concept is chosen because it applies to both sexually and asexually reproducing specimens, morphological and molecular characters, and it is commonly used by taxonomists.

Molecular Markers and Species Boundaries

The mitochondrial DNA (mtDNA) of animals is, with few exceptions, maternally inherited, and lacks recombination (Dawid & Blackler 1972; Wilson *et al.* 1985). The mitochondrial genome of insects is rather small (15-20kbp), circular, and has a relatively conserved gene arrangement (Avise *et al.* 1987; Boore 1999). The mutation rate is high due to a less stringent repair system (Wilson *et al.* 1985), which in many cases results in a high number of informative sites for species discrimination. Each cell usually contains many mitochondria, resulting in a relatively high number of mtDNA molecules in total DNA extracts, even from small organisms or samples. In technical terms this makes it easy to work with mtDNA, especially since there are 'universal' primers available that frequently work on 'new' taxa that have never been studied before. Many studies have shown that sequences of the mitochondrial cytochrome c oxidase subunit 1 (CO1) successfully separate closely related insect species (e.g. Clark *et al.* 2001; Li *et al.* 2010; Germain *et al.* 2013).

As of 2014, there are almost 1.6 million described species in the world, (Roskov *et al.* 2014), and estimates of the total number of species, including those still undescribed, range from 2 to 8 million species (Costello *et al.* 2013). Due to the large number of species that may be unknown to science, it is necessary to speed up and simplify the methods for identification, and DNA barcoding may be an appropriate tool (Waugh 2007). DNA barcoding refers to the use of a standardized genetic sequence that is linked to voucher specimens of known species. CO1 is commonly used for this purpose, and was first proposed by Hebert *et al.* (2003) to be a suitable marker for use in the barcoding project. This use of a single gene to identify species has been much debated (Moritz & Cicero 2004; Hebert & Gregory 2005; Elias *et al.* 2007; Hajibabaei *et al.* 2007; Waugh 2007; Whitworth *et al.* 2007). In order to use this approach to examine species boundaries, it is necessary to agree upon a standard 'species delimiter'. Hebert *et al.* (2004) suggested a threshold for interspecific difference ('the barcoding gap') of ten times the average intraspecific difference to delimit species. This has also been highly debated and tested in many lineages (Meyer & Paulay 2005; Hickerson *et al.* 2006; Rubinoff *et al.* 2006; Whitworth *et al.* 2007). In some insect orders there are issues with this method (Meier *et al.* 2006; Wiemers & Fiedler 2007; Meier *et al.* 2008), but so far it looks unproblematic for coleopterans (Cognato 2006).

Given the limitations of mtDNA it has been recommended to include at least one nuclear marker in molecular studies in order to track effects of incomplete lineage sorting or hybridization (Hebert *et al.* 2003). The internal transcribed spacer (ITS) 2 of the nuclear ribosomal gene cluster has also been shown to be suitable for separating species in certain insect linages (Hackett *et al.* 2000). The ITS regions are non-coding regions separating the ribosomal subunits 18S and 5.8S (or equivalents), and 5.8S and 28S (or equivalents) (Hillis & Davis 1986).

Since morphological identification of species of the genus *Mocyta* is difficult, molecular markers may be useful for this purpose. However, this has not been tested yet. From previous studies, some sequences of mitochondrial CO1 and mitochondrial cytochrome c oxidase subunit 2 (CO2) genes are available for *M. fungi* and *M. scopula* (Elven *et al.* 2010), making it possible to design optimized primer pairs targeting the most informative regions for species identification within these markers.

Purpose of this Study

Due to the lack of modern revisions of the tribe Athetini, and by extension the genus *Mocyta*, it is necessary to do a thorough examination of all currently available publications concerning the genus to determine which species are currently regarded as members of *Mocyta*. It is interesting to test if molecular markers can be used to delimit these species, and if the currently accepted *Mocyta* species and the morphospecies that can be recognized based on morphology are supported by these markers. Due to the widespread distribution of *Mocyta fungi*, it is also possible to investigate whether there is any geographic structure reflected in the genetic variation of *Mocyta fungi*, and if this variation corresponds to different ecological preferences. It is also interesting to examine if the parthenogenetic populations of *M. fungi* are restricted geographically. Summed up, in this study the following hypotheses are tested:

H1: The species of *Mocyta* that can be recognized based on morphology differ genetically.

H2: There is, in general, significant genetic variation among different Norwegian populations, and among European populations of *Mocyta fungi.*

H3: There is geographic structure in the genetic variation of *M. fungi*.

H4: The genetic variation of *M. fungi* corresponds to different ecological preferences.

H5: The parthenogenetic populations of *M. fungi* are restricted geographically.

Material and Methods

The Species of the Genus *Mocyta*

Based on a detailed investigation of publications regarding *Mocyta* species, an overview of the species of *Mocyta* has been compiled including species original combination, synonyms and a short diagnosis. The diagnoses were based on identification keys and species descriptions from various authors. The known distribution of the species was also examined, using catalogues, descriptions and web based records. In addition, some species were discussed more in detail.

Collecting Methods and Strategy

Different collecting methods were used to sample *Mocyta* specimens during the summer of 2012 and 2013 in several localities in southern Norway. In habitats with leaf and plant litter, a sifter was used to eliminate most of the litter but keep the insects (inevitably together with smaller particles). Specimens were extracted from the sifted material using one of the following three methods, depending on locality; (1) the sifted material was carefully examined by spreading a small portion of it on plastic sheet or in a plastic box, and individual specimens were collected with aspirator and placed in tubes with 96% ethanol; (2) most of the sifted material from the Oslo area was processed using Berlese funnels and collecting jars with 96% ethanol; (3) when sampling in Rogaland and Hordaland Winkler funnels were used, and the content of the collecting jars was sorted on a plastic sheet.

The sampling localities were selected to cover as many habitats as possible, ranging from dry to wet environments, from open landscape to dense vegetation, from low to high elevation, from highly disturbed to relatively undisturbed areas. In total, 54 localities were sampled; see Table 17 in 'Appendix 1: Specimens' and Figure 1 for details.

Sorting Collected Samples

The collecting jars from the Berlese funnels contained both invertebrates and large amounts of debris. These samples were sorted using a Leica Wild MZ8 binocular microscope, and all staphilinids were put aside for further identification. The residue was transferred to separate tubes with 100% ethanol for long term storage in freezer.

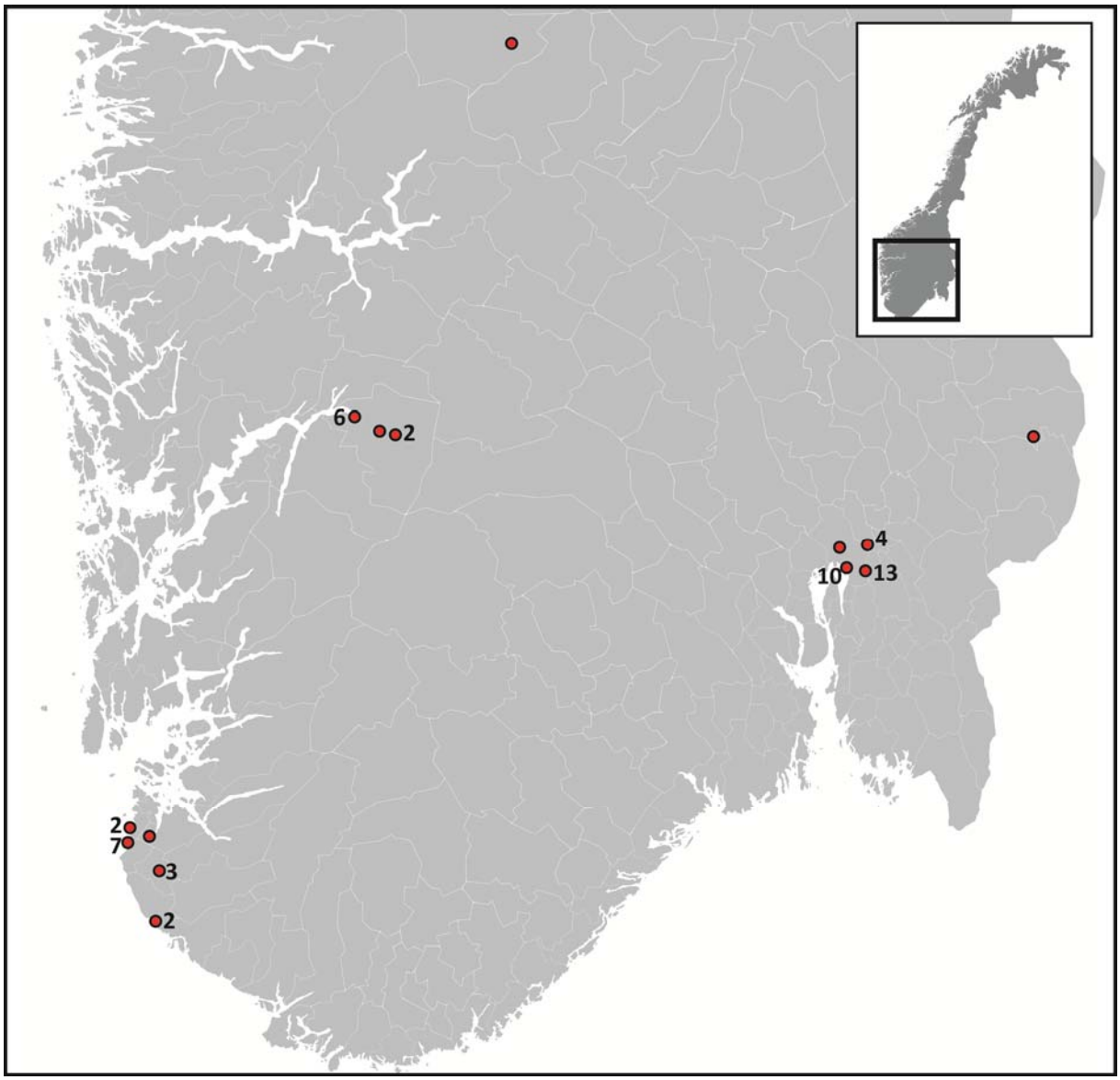


Figure 1: Map of Southern Norway showing the 54 sampled localities (red dots). Dots covering more than one locality are marked with a number of total localities. Illustration by the author based on vector map "Norway municipalities 2012 blank.svg" by Røed licensed under CC BY-SA 2.0 (2011).

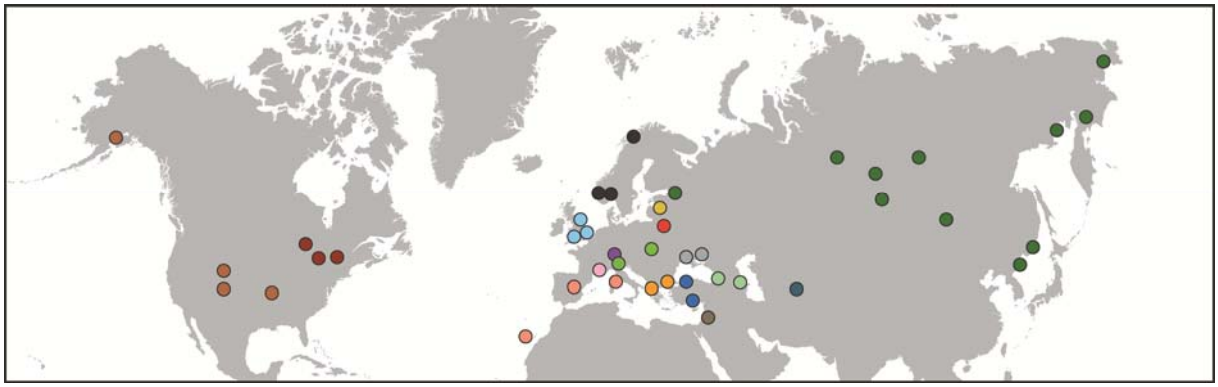


Figure 2: Map showing approximate localities for included samples. From some localities several samples where included. Dots are coloured based on country and match the colours used to separate countries in other illustrations. Illustration by the author based on label information of the samples selected and marked on "World map - low resolution.svg" by Al MacDonald licensed under CC BY-SA 3.0 (2009).

Identification

Specimens belonging to the subfamily, tribe and genus of interest (Aleocharinae, Athetini, *Mocyta* (and allies), respectively) were separated from other staphylinids using simplified diagnoses (Table 1). All *Mocyta* specimens were then identified to species using available keys and descriptions (Brundin 1952; Benick & Lohse 1974).

Table 1: Simplified diagnosis of subfamily Aleocharinae, tribe Athetini and genus *Mocyta*.

Step	Character	Identification (next step)
1.	Antenna inserted on top of head, not on the front edge	Subfamily Aleocharinae (2)
2.	Tarsal formula 4-5-5	Tribe Athetini (3)
3.	No hypomeron (epipleuron) visible in lateral view	Genus *Mocyta* and "allies" (Brundin's key)

Specimen Selection

When selecting specimens for DNA extraction, the process was guided by three criteria; to include all *Mocyta* species available, to cover the range of possible intraspecific variation and to select a sufficient number of specimens. Additional specimens from the existing DNA grade insect collection at the Natural History Museum were selected and identified by Vladimir Gusarov. These included some specimens collected in the United Kingdom by Peter Hammond and in Ukraine by Nikolai Yunakov. In total, 161 specimens were selected for DNA extraction, 32 newly collected in the field and 129 from the existing museum collection (see **Feil! Fant ikke referansekilden.** for approximate localities for included samples). Based on morphology, Vladimir Gusarov sorted the material into 14 morphospecies groups, of which some were identified to species level. The groups that could not be unambiguously assigned to a named species were numbered as Mocyta species 2 through Mocyta species 7.

Specimen Preparation

All specimens selected for DNA extraction were prepared by dividing the beetles into three parts; (1) head and prothorax for extraction and subsequent vouchering, (2) meso- and metathorax for preservation in the DNA grade collection in case re-extraction is needed, and (3) abdomen for genitalia extraction and vouchering. The head and prothorax were transferred into labelled Eppendorf LoBind® tubes with a drop of ethanol. The meso- and metathorax were transferred back to the original tube filled with 100% ethanol. The abdomen was treated with 10% solution of potassium hydroxide (KOH) to dissolve soft tissues, after which the abdomen was rinsed thoroughly in water. The genitalia were

extracted and transferred to genitalia vials with a drop of glycerine. The abdomen was mounted on 11 x 5 mm pinned glue boards and labelled. For full list of specimens and labels see Table 18 in 'Appendix 1: Specimens'.

DNA Extraction

DNA extraction was carried out at the DNA lab at the museum using DNEasy Blood & Tissue Kit (Qiagen 2006) and following manufacturer's protocol for animal tissue with minor modifications as described in Elven *et al.* (2010). The ethanol was removed from the samples, first by use of pipette, and then by vacuum drying. Beetle exoskeletons were left in the Eppendorf tubes after DNA extraction, and were later rinsed in water and mounted on the glue boards together with the respective abdomens. The remaining genomic DNA extracts were deposited at the NHM in Oslo.

Primer Testing and DNA Amplification

Several primer pairs for CO1 were tested on some of the samples to find a pair that worked with as many samples as possible. Additionally, primers targeting overlapping shorter fragments (~ 200bp) of CO1 were tested on older specimens with degraded DNA. Primer pairs targeting ITS1 and ITS2 were also tested. For details on the primers used see Table 19 in 'Appendix 2: Primers'.

The 25µl reaction mixture in which the PCR (Polymerase Chain Reaction) was run contained 2.5mM $MgCl_2$, 1X PCR buffer II (Applied Biosystems®), 0.8mM GeneAmp dNTP Mix (Applied Biosystems®), 1U AmpliTaq® DNA Polymerase (Applied Biosystems®), 0.5µM of each primer and 3µl of the respective DNA extract.

The following PCR program was used for all samples and primer pairs: starting with an initialising step at 94°C for 30 seconds, followed by 35 cycles of denaturation (94°C for 1 minute), annealing (50°C for 30 seconds) and elongation (72°C for 2 minutes), finished by a final elongation at 72°C for 10 minutes before the final hold at 4°C. The annealing temperature was adjusted as necessary, see primer table (Table 19 in 'Appendix 2: Primers') for more details.

PCR products were checked using gel electrophoresis with Biotium GelRed™ as fluorescence tag.

Cleaning and Sequencing

The PCR products were cleaned using illustra™ ExoStar™ 1-Step (GE Healthcare Life Sciences 2011), following the manufacturer's protocol for 14µl total volume. The strips were then incubated in the PCR machine using the following program: 45 minutes at 37°C for the two enzymes (illustra Alkaline Phosphatase and Exonuclease 1) to break down unincorporated primers and nucleotides, followed by 15 minutes at 80°C for denaturation of the enzymes.

All samples were prepared for sequencing at StarSEQ GmbH, following the manufacturer's instructions for 'U-mix', and diluting samples that yielded much PCR product 1:1 with distilled water from the Millipore tap. The marked strips were packed and sent to StarSEQ GmbH for sequencing. Trace files were received by e-mail.

Trimming and Assembling

The assembling was done automatically in CodonCode Aligner v. 4.2.7 (CodonCode Corporation 2014), using standard options, and the primer regions were manually trimmed from all sequences. Each sequence was checked for errors and unreliable areas. All sequences were exported and loaded into a MySQL database (for details se the section 'Data Management'). Only samples that yielded sequences for both CO1 and ITS2 were later retrieved from the database for further analyses.

Aligning

Aligning the CO1 sequences was straightforward. The ITS2 sequences, on the other hand, were harder to align with confidence due to high variation. The ITS2 sequences from the outgroup taxa were so different from the *Mocyta* sequences that they were removed prior to aligning. First, the sequences were aligned using the *Muscle* algorithm (Edgar 2004) implemented in *MEGA6* (Tamura *et al.* 2013) with gap penalties set to the default -400 for 'open' and 0 for 'extend', clustering method was set to 'Neighbor Joining' and minimum length of the diagonal ('lambda') was set to, by default, 24. Changes in these settings did not improve the alignment significantly, so some segments were edited manually, and, due to ambiguity, a region of 14 bases was removed (bases 296-310) from all sequences.

Analysing

Datasets

For the analyses two main datasets were generated that included all samples which yielded both CO1 and ITS2 sequences, one for each marker (CO1 dataset and ITS2 dataset). Additional datasets, one per marker, were generated for each of the identified morphospecies represented by three or more sequences that were not identical, in total nine datasets, six CO1 datasets and three ITS2 datasets.

Neighbor-Joining Trees

Trees were produced for both of the main datasets using the Neighbor-Joining (NJ) method (Saitou & Nei 1987) as implemented in *Mega* 6 (Tamura *et al.* 2013). Substitution type 'Nucleotide' including transitions and transversions was used, calculated using the p-distance method. 'Rates among sites' was set to 'uniform' and 'pattern among linages' as 'homogeneous'. 'Pairwise deletion' was selected for treatment of gaps and missing data. The phylogeny was tested by 1000 bootstrap replications.

Model Tests

For model-based analyses of the DNA alignments, a nucleotide substitution model was selected for each alignment using *jModelTest 2* (Guindon & Gascuel 2003; Darriba *et al.* 2012). First the likelihood scores were calculated using the default settings: 11 substitution schemes (NumModels=88), under 'Base frequencies' '+F' was checked, '+I' and '+G' was checked under 'Rate variation' (nCat=4), the base tree was set to 'ML optimized' and NNI as tree searching method. The user may choose between three different information criteria: AIC (Akaike information criterion), BIC (Bayesian information criterion) or a performance based method based on decision theory (DT). BIC and AIC were used for both ITS2 and CO1, with default settings, to find the best model.

Maximum Likelihood

Maximum Likelihood (ML) analyses were run in *PhyML 3* (Guindon *et al.* 2010) using the command lines suggested by *jModelTest 2* for the best models, only adding bootstrap replications (1,000).

Bayesian Inference

MrBayes 3 (Huelsenbeck & Ronquist 2001; Ronquist & Huelsenbeck 2003) was used for the Bayesian inference (BI) analyses. A Generalized Time Reversible (GTR) substitution model was selected for the CO1 dataset. Based on the model selection (see above and 'Results'), the parameter '`invgamma`' (a proportions of the sites are invariable, the remaining has gamma-distributed rate variation) was activated (GTR+G+I). For the ITS2 dataset a symmetrical model with a proportion of invariable sites (SYM+I) (Zharkikh 1994) was used. 'Metropolis-coupled Markov chain Monte Carlo' (MCMCMC) was run with four chains (one cold and three heated), and four independent analyses simultaneously for an initial 2,000,000 generations with sample frequencies set to 200, see scripts in Figure 3 and Figure 4. If convergence was reached after these generations the analysis was stopped, if not the analysis was set to continue for additional generations. This step was repeated until the 'average standard deviation of split frequencies' reached a low value that did not change significantly between calculations of MCMC diagnostics (set to run each 5,000 generation).

A summary for the sample of substitution model parameters was run using the command '`sump`', and summary for the samples of trees and branch lengths with the command '`sumt`'. Burn-in was set to 25% for both summaries.

```
BEGIN mrbayes;
lset nst=6 rates=invgamma;
mcmc ngen=2000000 nchains=4 nruns=4 samplefreq=200
  printfreq=200 savebrlens=yes;
END;
```

Figure 3: Script added to the end of the NEXUS-formatted (Maddison *et al.* 1997) **CO1 alignment prior to analyses in *MrBayes* (substitution model GTR+I+G).**

```
BEGIN mrbayes;
lset nst=6 rates= propinv;
prset statefreqpr=fixed(equal);
mcmc ngen=2000000 nchains=4 nruns=4 samplefreq=200
  printfreq=200 savebrlens=yes;
END;
```

Figure 4: Script added to the end of the NEXUS-formatted (Maddison *et al.* 1997) **ITS2 alignment prior to analyses in *MrBayes* (substitution model SYM+I).**

Intra- and Interspecific Genetic Variation

For both the main datasets the overall genetic distance was measured in addition to the mean intra- and interspecific distance, using *MEGA6*. Distance estimations were performed using the Kimura 2-parameter model (K2P) (Kimura 1980) with gamma distribution parameter equal to the value used in the ML-analyses (0.663 for the CO1 dataset and none for the ITS2 dataset). Bootstrap with 1,000 replications was used as variance estimation method, and with pairwise deletion of gaps and missing data. In both datasets the sequences were grouped in three different ways: according to the marked clades in Figure 10 and Figure 11, respectively for each marker (CO1 clade dataset and ITS2 clade dataset); according to the species identified by Vladimir Gusarov (CO1 morphospecies dataset and ITS2 morphospecies dataset); and finally, based on the smallest monophyletic clades using a maximum threshold of 0.2 expected changes per site for CO1 and 0.02 for ITS2 to maintain some genetic distance within groups (CO1 SMC dataset and ITS2 SMC dataset).

The online service bPTP (Poisson Tree Processes with Bayesian support (Zhang *et al.* 2013)), available at http://species.h-its.org/ptp/, was used on both trees from the BI analyses as an additional method for delimiting species. Estimations based on the CO1 BI tree were run with the following settings: rooted with 100,000 MCMC generations; thinning set to 100; and burn-in set to 0.1. Estimations based on the ITS2 BI tree were run using the same settings, but for unrooted tree.

Haplotype Networks

Each of the additional datasets (see above) was edited (removing congruent gaps) using *PhyDE®* (Müller *et al.* 2010). The edited additional datasets were imported to *MEGA6* for generation of quick NJ-trees. The datasets were then imported to *HaploViewer* (Salzburger *et al.* 2011) together with the corresponding NJ-tree. The program was set to differentiate according to country, so that each haplotype was illustrated as pie charts with colours identifying the country. The two main datasets were also analysed using *HaploViewer* to assign a haplotype number to each specimen. The haplotype numbers were loaded into the MySQL database (see below) and the haplotypes for the newly collected *Mocyta fungi* specimens (from southern Norway) were exported to visualise the geographical distribution of each haplotype using *Highcharts* (Highsoft AS 2014).

Data Management

For easy retrieval and tracking of all samples and their respective sequences, all information for each sample was loaded into a *MySQL 5.6* (MySQL 2013) database. The label information for each sample (including collecting date, taxon name, locality and geographic coordinates, information about habitat and surrounding vegetation) was available in a spreadsheet created while sorting the sampled material. This information was divided into columns and imported to the database (see Figure 17: 'specimens' in 'Appendix 6: Data Management' for details). The primer information was loaded in a separate table, see Figure 17: 'primers'. A separate table was also created for the abbreviations used for the samples when sending to StarSeq (Figure 17: 'sequences'), with reference to strip codes for PCR product kept at the DNA lab at the museum. Finally, all the sequences were added to separate tables based on marker (Figure 17: 'co1_contig' and 'its2_contig'), including both raw and aligned sequences. For easy editing and updating of the database *Navicat for MySQL* (PremiumSoft CyberTech Ltd. 2014) was used.

Using *node.js* (Dahl *et al.* 2014) the information of interest was easily retrieved from the database and printed in desired format. All FASTA files used for analyses were made using node scripts, see Figure 18 in 'Appendix 6: Data Management' as an example of a script making FASTA file containing aligned CO1 sequences.

Results

The Species of the Genus *Mocyta*

Mocyta fungi (Gravenhorst, 1806)

Original combination: *Aleochara fungi* Gravenhorst, 1806.

Synonyms: *Bolitochara agaricola* Mannerheim, 1830*; Aleochara infuscata* Stephens, 1832*; Aleochara obfuscata* Stephens, 1832*; Aleochara xanthopa* Stephens, 1832*; Homalota cingulata* Heer, 1839*; Oxypoda myrmecobia* Mannerheim, 1843*; Homalota hygrophila* Hardy, 1851*; Homalota rhyssoptera* Kraatz, 1859*; Oxypoda modesta* Motschulsky, 1860*; Oxypoda praecox* Hochhuth, 1862*; Homalota dubia* Sharp, 1869*; Colpodota laeticornis* Mulsant & Rey, 1873*; Coplodota simulans* Mulsant & Rey, 1873*; Colpodota ciligera* Mulsant & Rey, 1874*; Achromata fusiformis* Casey, 1893*; Acrotona adjuvans* Casey, 1910*; Acrotona lividula* Casey, 1910*; Dimetrota nuptalis* Casey, 1910*; Acrotona beskidica* Pasnik, 1999*; Acrotona forestica* Pasnik, 1999*; Acrotona otrytica* Pasnik, 1999.

Invalid combinations: *Atheta fungi* (Gravenhorst, 1806); *Acrotona fungi* (Gravenhorst, 1806); *Homalota fungi* (Gravenhorst, 1806).

Diagnosis: The species is small and slender, 2.4-2.8 mm long, glossy black to brown-black often with lighter posterior edges of the pronotum, elytra and abdominal terga. The legs are yellow or brown-yellow. The head is clearly smaller than the pronotum, and in lateral view the eyes are approximately of the same length as the temples. The antennae are yellow-brown to brown, and lighter at the base. The 1st to 7th antennal segments are slightly elongate or square, and from the 8th to the 11th slightly transverse. The pronotum is 1⅕ times wider than long, arched, widest at or behind the middle, and has fine and dense punctation. The elytron widens posteriorly and is slightly narrower than the pronotum anteriorly. Measured at the suture, i.e. from the tip of the scutellum to posterior margin, the elytra are normally shorter than the pronotum and slightly denser and more distinctly punctured. Punctation of the abdomen is fine and rather dense, posteriad it is more sparsely and coarsely punctured. The 8th tergite is blunt in both sexes, and the 8th sternite of males is tapered. The absolute length of the spermatheca (see Figure 7) is approximately 0.25 mm (Brundin 1952; Palm 1970; Benick & Lohse 1974). See Figure 8 for illustration of *M. fungi*.

Geographical distribution: *Mocyta fungi* is the most widespread of all the *Mocyta* species, recorded in almost all of Europe, large parts of North Africa, all of Russia, several

countries in Asia, and also introduced to North America (Löbl & Smetana 2004; Silfverberg 2004), see Figure 6A for details.

Distribution in Norway: According to the data provided by the Natural History Museum UIO (NHM), BioFokus, Norwegian institute for nature research (NINA), NTNU University Museum and Norwegian entomological society (NEF) through the online service Artskart 1.6 (Artsdatabanken & GBIF-Norge 2014), *M. fungi* is widespread in Norway, recorded in all the nineteen mainland counties. The number of specimens at NHM also indicates that this is the most common species of *Mocyta.* Tor Helliesen (1914) reported the species to be '*exceedingly common*' everywhere in Rogaland.

Red list status in Norway: Least concern (LC).

Discussion: The species is very variable in morphological characters (Benick & Lohse 1974; Topp 1975; Lohse *et al.* 1990). Based on museum collections the population in Norway seems to be mainly parthenogenetic; this might also be the case for non-Norwegian populations (Topp 1974; Lohse & Smetana 1985). The spermatheca varies between individuals, even between individuals descending from the same female (see Figure 5), and has no reliable characters for identification (Brundin 1952; Topp 1975). Many of the species in the genus *Mocyta* have earlier been proposed to be varieties of *M. fungi* (i.e. *fungi var. amplicollis*, *fungi var. clientula*, *fungi var. orbata*), but Lohse and Smetana (1985) argue that due to their different reproduction strategies (*M. fungi* being parthenogenetic and the others bisexual) this cannot be the case.

Figure 5: Illustration from (Topp 1975, fig. 4) showing the spermatheca from six mothers (*P*) compared with the spermatheca of their daughters (F_1).

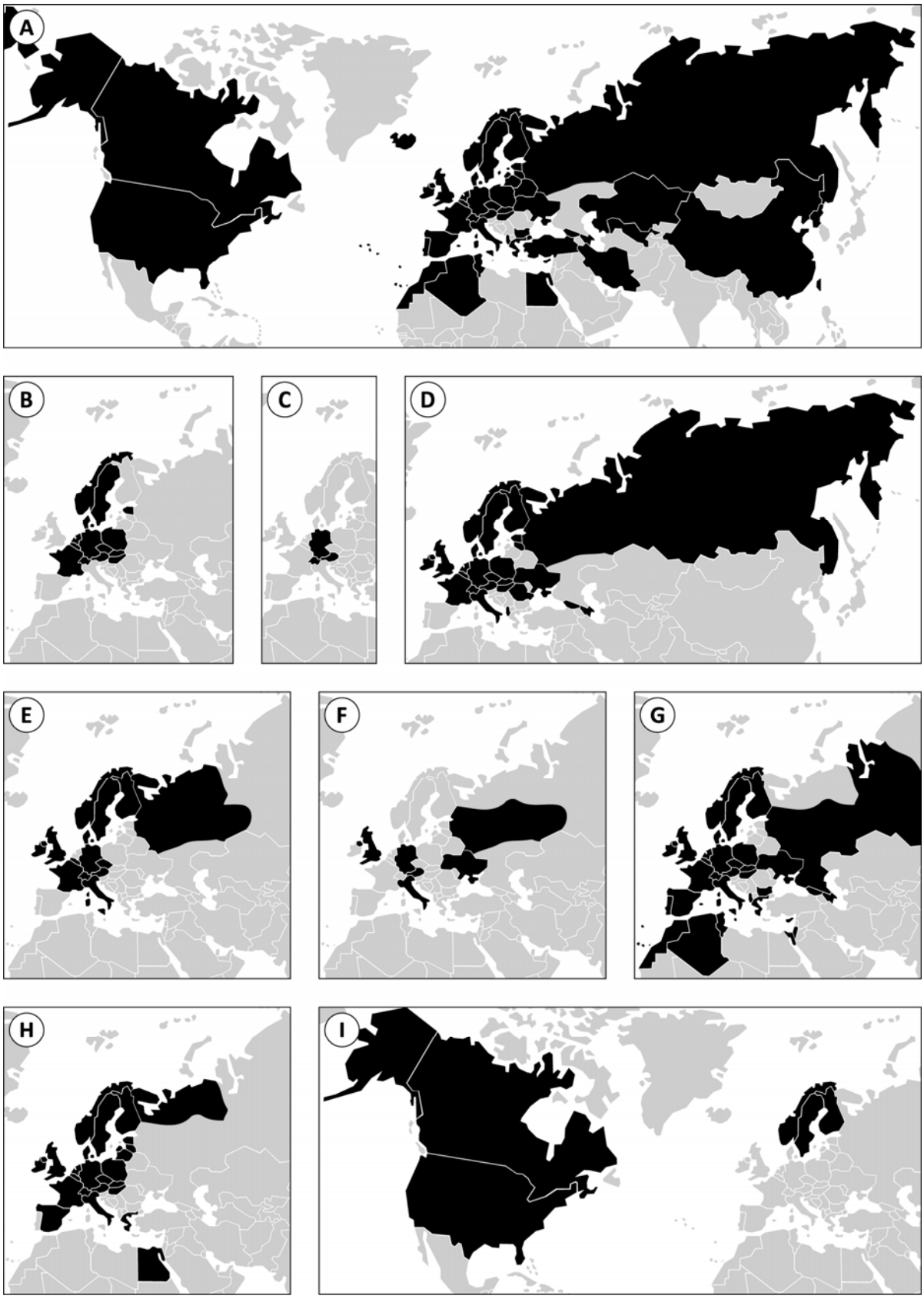


Figure 6: Distribution at country level of some *Mocyta* species: *Mocyta fungi* (A), *M. negligens* (B), *M. gilvicollis* (C), *M. orphana* (D), *M. amplicollis* (E), *M. fussi* (F), *M. clientula* (G), *M. orbata* (H), *M. amblystegii* (I). Black demotes countries where the specific species is recorded. Illustrations by the author, distribution based on Löbl & Smetana (2004) and Silfverberg (2004) mapped on "World map - low resolution.svg" by Al MacDonald licensed under CC BY-SA 3.0 (2009)

Mocyta amplicollis (Mulsant & Rey, 1873)

Original combination: *Colpodota amplicollis* Mulsant & Rey, 1873.

Invalid combinations: *Atheta amplicollis* (Mulsant & Rey, 1873); *Atheta fungi var. amplicollis* (Mulsant & Rey, 1873).

Diagnosis: The beetles are larger than *M. fungi*, 2.7-3.0 mm long and dark coloured. The pronotum is larger and more massive than in the other species, almost 1½ times wider than long, and much wider than the elytra at the shoulders. *Mocyta amplicollis* is distinguishable from *M. amblystegii* by being lighter coloured and having light brown antennae (at least at the base). All antennal segments are elongate, and the 11th segment is much longer than the 9th and 10th together (Benick & Lohse 1974). For illustration of genitalia see Figure 7.

Geographical distribution: *Mocyta amplicollis* is represented mainly in Western and Northern Europe (Löbl & Smetana 2004; Silfverberg 2004), see Figure 6E for details.

Distribution in Norway: Andreas Strand (1968) listed the species occurrences in Lommedal, Akershus; Røa, Oslo; Svene, Buskerud; Mo i Rana and Lødningen, Nordland; and Målsnes, Troms. The species is also recorded by NINA (Norsk institutt for naturforskning) in Lindås, Hordaland. The data are available at Artskart 1.6 (Artsdatabanken & GBIF-Norge 2014).

Red list status in Norway: Least concern (LC).

Discussion: Mulsant and Rey (1873) described the species as a variant of *M. fungi*. First time listed as member of (subgenus) *Mocyta* in Benick & Lohse (1974).

Mocyta amblystegii (Brundin, 1952)

Original combination: *Atheta amblystegii* Brundin, 1952.

Invalid combinations: *Atheta amblystegii* Brundin, 1852; *Acrotona amblystegii* (Brundin, 1852).

Diagnosis: These beetles, like *M. amplicollis*, are larger than *M. fungi*, 2.7-3.0 mm long and dark coloured. The pronotum is larger and more massive than in the other species, almost 1½ times wider than long, and much wider than the elytra at the shoulders. *Mocyta amblystegii* is distinguishable from *M. amplicollis* by its black-coloured body and antennae. The legs are also dark, but with brighter tarsi. The 11th segment is barely as long as the 9th and 10th together (Brundin 1952; Palm 1970; Benick & Lohse 1974; Lohse *et al.* 1990). For illustration of genitalia see Figure 7.

Geographical distribution: This species occurs in Norway, Sweden and Finland, and probably has circumpolar distribution, because it is also registered in the Nearctic (Löbl & Smetana 2004; Silfverberg 2004), see Figure 6I for details.

Red list status in Norway: Least concern (LC).

Discussion: First time listed as member of (subgenus) *Mocyta* by Benick and Lohse (1974).

Mocyta orbata (Erichson, 1837)

Original combination: *Homalota orbata* Erichson, 1837.

Invalid combinations: *Atheta orbata* (Erichson, 1837); *Atheta fungi var. orbata* (Erichson, 1837); *Acrotona orbata* (Erichson, 1837); *Homalota orbata* Erichson, 1837.

Diagnosis: The body is more slender and less curved than *M. fungi*, and is darker and has more distinct side bristles. The head and pronotum appear very glossy due to the delicate punctation and microsculpture. The pronotum is often lighter coloured than the rest of the body, barely 1⅓ times wider than long with conspicuous side bristle. The elytra are often lighter coloured. The antennae are robust and dark brown. The basal antennal segment is dark and enlarged, and all the other segments are short and clearly transverse. The legs are yellow-brown and the middle femur has a short bristle. The body is 2-3 mm long (Brundin 1952; Palm 1970; Benick & Lohse 1974). For illustration of genitalia see Figure 7.

Geographical distribution: The species is registered in almost all countries in Europe, and in addition, in Egypt (Löbl & Smetana 2004; Silfverberg 2004), see Figure 6H.

Distribution in Norway: Data provided by the NHM, BioFokus, NINA and NTNU University Museum through the online service Artskart 1.6 (Artsdatabanken & GBIF-Norge 2014) show that *M. orbata* is, like *M. fungi*, represented in all the mainland counties in Norway. Tor Helliesen (1914) reported the species to be found on moss above the sand dunes of Jæren, Rogaland, but not common.

Red list status in Norway: Least concern (LC).

Discussion: First time listed as member of (subgenus) *Mocyta* in Benick & Lohse (1974).

Mocyta orphana (Erichson, 1837)

Original combination: *Homalota orphana* Erichson, 1837.

Synonyms: *Colpodota nigricolor* Mulsant & Rey, 1874.

Invalid combinations: *Acrotona orphana* (Erichson, 1837); *Atheta orphana* (Erichson, 1837); *Homalota orphana* (Erichson, 1837).

Diagnosis: The species is very similar to *M. fungi*, but smaller, only 1.6-2 mm long and has a wider pronotum, nearly 1½ times wider than long and more narrowing anteriorly. The elytra have dense punctation and are strongly convex at the posterior margins adjacent to the outer corners. Measured at the suture, the elytra are as long as the pronotum. The antennae are black-brown and robust, with a yellow or light brown and noticeably thickened basal segment. The penultimate antennal segment is 1½ times wider than long. The abdomen is black and the legs yellow-brown (Brundin 1952; Palm 1970; Benick & Lohse 1974). For illustration of genitalia see Figure 7.

Geographical distribution: This is one of the most widespread of the *Mocyta* species, registered in nearly all European countries, and most of Russia (Löbl & Smetana 2004; Silfverberg 2004). See Figure 6D for details.

Distribution in Norway: Through the online service Artskart 1.6 (Artsdatabanken & GBIF-Norge 2014) NHM and NTNU Vitenskapsmuseet report specimens collected in seven of the Norwegian counties: Finnmark, Nordland and Troms in the northern parts, Oppland and Sør-Trøndelag in the central parts and Buskerud, Vest-Agder and Vestfold in the southern parts. Tor Helliesen (1914) reported the species to be common on moss above the sand dunes of Jæren, Rogaland.

Red list status in Norway: Least concern (LC).

Mocyta negligens (Mulsant & Rey, 1873)

Original combination: *Colpodota negligens* Mulsant & Rey, 1873.

Invalid combinations: *Acrotona negligens* (Mulsant & Rey, 1873); *Atheta negligens* (Mulsant & Rey, 1873).

Diagnosis: The species is light coloured, with light reddish brown to brown-yellow elytra and light coloured antennae. The 5th antennal segment is as wide as it is long, and the penultimate segment almost 1½ times wider than long. The aedeagus and spermatheca are about 2/3 the size of those of *M. fungi*. *Mocyta negligens* is distinguishable from *M. gilvicollis* by the 11th antennal segment being as long as the 9th and 10th together. The body is 1.8-2.4 mm long (Benick & Lohse 1974). For illustration of genitalia see Figure 7.

Geographical distribution: *Mocyta negligens* is recorded in Central and Northern parts of Europe (Löbl & Smetana 2004; Silfverberg 2004), for details see Figure 6B.

Distribution in Norway: It is assumed that reproducing populations are present in temperate broadleaf forests in Oslo and Akershus, as suggested by the findings after 1980 (Kålås *et al.* 2010).

Red list status in Norway: Near threatened (NT) (Kålås *et al.* 2010).

Mocyta gilvicollis (Scheerpeltz, 1949)

Original combination: *Atheta gilvicollis* Scheerpeltz, 1949.

Invalid combinations: *Acrotona gilvicollis* (Scheerpeltz, 1949); *Atheta gilvicollis* Scheerpeltz, 1949.

Diagnosis: The species is larger, 2.5-2.7 mm long, wider and lighter coloured than *M. negligens*. The elytra are light reddish brown to brown-yellow, and both the antennae and elytra are longer. The basal antennal segment is reddish-yellow, antennae gradually darker and slightly thickening from the 5th segment to the apex. The penultimate antennal segment is about 1⅓ times wider than long. *Mocyta gilvicollis* is distinguishable from *M. negligens* by the 11th segment being much longer than the 9th and 10th together (Scheerpeltz 1949; Benick & Lohse 1974). See Figure 8 for illustration of *M.gilvicollis.*

Geographical distribution: *Mocyta gilvicollis* is the *Mocyta* species with most limited distribution, only reported in three countries: Austria, Germany and Switzerland (Löbl & Smetana 2004; Silfverberg 2004), see Figure 6C for details.

Mocyta clientula (Erichson, 1839)

Original combination: *Homalota clientula* Erichson, 1839.

Synonyms: *Homalota pulchra* Kraatz 1856; *Homalota montivagans* Wollaston, 1857; *Homalota aleocharoides* Wollaston, 1864; *Homalota sharpi* Rye, 1870.

Invalid combinations: *Atheta clientula* (Erichson, 1839); *Acrotona clientula* (Erichson, 1839); *Homalota clientula* (Erichson, 1839); *Colpodota clientula* (Erichson, 1839); *Atheta fungi* var*. clientula* (Erichson, 1839).

Diagnosis: The species is larger, 2.3-3.2 mm long, wider and lighter coloured than *M. orbata*. The head and pronotum appear very glossy due to the delicate punctation and microsculpture. The antennae are robust and brown, rarely or barely lighter at the base.

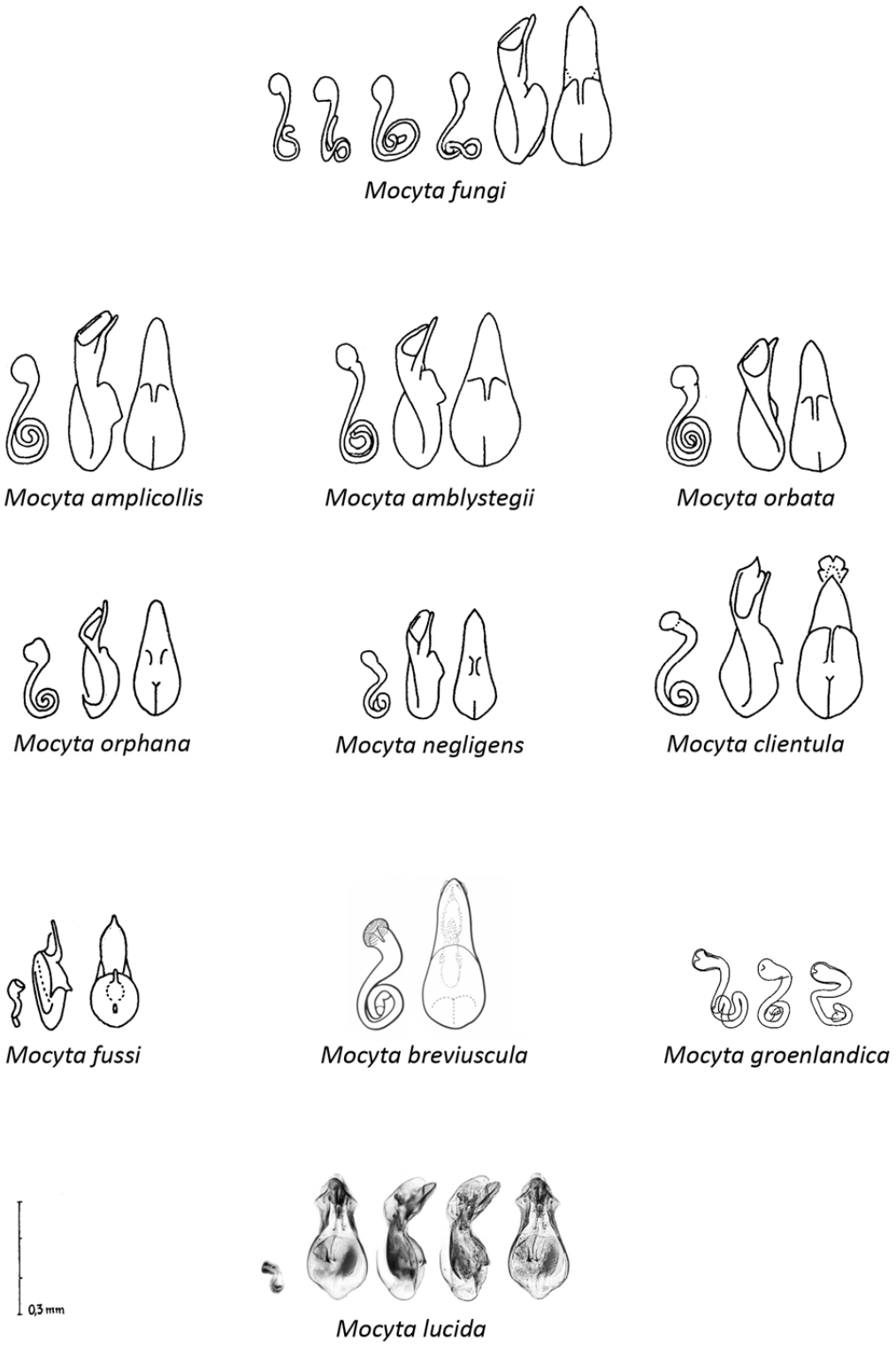


Figure 7: Illustrations of spermathecae (left) and aedeagi (right) of some *Mocyta* species. Illustrations of *M. breviuscula* by Lohse & Smetana (1985, fig. 17–18), *M. groenlandica* by Mahler (1988, fig. 13–15), *M. lucidia* by Renner & Tronquet (2013, fig. 2), and the rest are by Benick & Lohse (1974, p. 181–182). All illustrations are scaled according to the scale of Benick & Lohse (1974).

The pronotum is almost 1½ times wider than long with conspicuous side bristles and light brown colour. The elytra are often two-coloured, darker colour encircling the scutellum and bordering the outer anterior corners. The legs are yellow and have a long bristle on the middle and hind femur (Brundin 1952; Palm 1970; Benick & Lohse 1974). For illustration of genitalia see Figure 7.

Geographical distribution: *Mocyta clientula* is widespread, registered in North Africa, Europe and large parts of Russia, see Figure 6G for details.

Distribution in Norway: It is assumed that reproducing populations exist in constructed land and semi-natural grasslands in Østfold based on recorded occurrences prior to 1980 (Kålås *et al.* 2010). There is one registered occurrence from Hvaler in Østfold from 1926 in the collection at NHM.

Red list status in Norway: Endangered (EN) (Kålås *et al.* 2010).

Mocyta fussi (Bernhauer, 1908)

Original combination: *Atheta fussi* Bernhauer, 1908.

Synonyms: *Homalota nitens* Fuss, 1868.

Invalid combinations*: Atheta fussi* Bernhauer, 1908; *Acrotona fussi* (Bernhauer, 1908); *Homalota fussi* (Bernhauer, 1908); *Colpodota fussi* (Bernhauer, 1908).

Diagnosis: The body is somewhat flattened, and the pronotum is 1½ times wider than long. The eyes are large, 1½ times larger than the temples. The antennae are short, black and shiny. The 3rd antennal segment is slim and much shorter than the 2nd segment and the penultimate antennal segment is transverse. The elytra are not rounded at the posterior margins adjacent to the outer corners. The body is 1.8-2 mm long (Benick & Lohse 1974). For illustration of genitalia see Figure 7.

Geographical distribution: According to the known distribution of *M. fussi* listed in the 'Catalogue of Palaearctic Coleoptera' by Löbl & Smetana (2004) the species occurs across Europe, see Figure 6F for details.

Mocyta breviuscula (Mäklin in Mannerheim, 1852)

Original combination: *Homalota breviuscula* Mäklin, 1852.

Synonyms: *Acrotona digesta* Casey, 1910; *A. severa* Casey, 1910; *A. shastanica* Casey, 1910; *A. prudens* Casey, 1910; *A. ardelio* Casey, 1910; *A. renoica* Casey, 1910, *A. malaca* Casey, 1910.

Invalid combinations: *Acrotona breviuscula* (Mäklin in Mannerheim, 1852); *Atheta breviuscula* (Mäklin in Mannerheim, 1852).

Diagnosis: Compared to *M. fungi* the species is smaller, and has smaller eyes. In dorsal view the eyes are clearly shorter than the temples. The antennae are more robust and smaller than those of *M. fungi*, and the pronotum is wider, almost as wide as the elytra. The midline of the pronotum and the sides of the elytra are the same size, or the pronotum is longer. The spermatheca is easily distinguished from that of *M. fungi* by having a much longer umbilicus. The length of the body is 2.1-2.5 mm (Lohse & Smetana 1985). For illustration of genitalia see Figure 7.

Geographical distribution: According to Lohse & Smetana (1985) the species is widespread in the North-Western parts of North America (Alaska in USA, and British Colombia and Alberta in Canada). It is also recorded in California and Nevada in USA (Gusarov 2003).

Discussion: The species was first listed in the genus *Mocyta* by Gusarov (2003) in his revision of some North American aleocharines.

Mocyta lucida (Dodero, 1922)

Original combination: *Atheta lucida* Dodero, 1922.

Invalid combinations: *Atheta lucida* Dodero, 1922.

Diagnosis: The beetles are black with very dark brown elytra, antenna and apical terga and light brown legs. The pubescence is very fine, short and sparse making the species very glossy. The head is large, just a little narrower than the pronotum, and has large eyes. The pronotum is 1½ times wider than long, is very lightly pubescent and has three long black side bristles. The punctation is also light. The elytra are clearly but sparsely punctured. The pubescence of the elytra is more distinct than that on the pronotum and the elytra have long black bristles on the shoulders. The abdomen has much longer microsetae than the elytra and the punctation is more distinct, especially on the last segments. The body of the beetle is about 1.7 mm long (Dodero 1922). For illustration of genitalia see Figure 7.

Geographical distribution: According to Renner & Tronquet (2013) the species occurs in northern Italy, the French Pyrenees and southern Germany.

Discussion: The species was first listed in the subgenus *Mocyta* in the genus *Atheta* by Renner and Tronquet (2013).

Mocyta scopula (Casey 1893)

Original combination: *Eurypronota scopula* Casey, 1893.

Synonyms: *Dolosota abundans* Casey, 1910; *D. flaccida* Casey, 1910; *D. redundans tergina* Casey, 1910; *D. secunda* Casey, 1910; *D. sequax* Casey, 1910; *Pancota laetabilis* Casey, 1911.

Invalid combinations: *Acrotona scopula* (Casey, 1893), *Eurypronota scopula* Casey, 1893.

Diagnosis: The species is flavo-testaceous (brownish red with a yellow tint) with black head and elytra a little darker and more brownish. *Mocyta scopula* is easily distinguishable from the other species of the genus by having a black spot on the fourth segment of the abdomen and a much lighter body colour (Casey 1893).

Discussion: Elven *et al.* (2010) were the first to include this species in the genus *Mocyta*.

Mocyta groenlandica (Mahler, 1988)

Original combination: *Atheta groenlandica* Mahler, 1988.

Diagnosis: The body is very dark in colour: black head, pronotum and abdomen, with lighter margins on the pronotum and posterior on abdominal segments. The elytra and antennae are brown. The basal antennal segment is almost black. The eyes are smaller than those of *M. fungi*, clearly shorter than the temples. The antennae are robust, and the penultimate segment is slightly more transverse than that of *M. fungi*. The microsetae on head and pronotum have the same pattern as *M. fungi*, but are more erect. The elytra strongly broaden posteriad. The spermatheca length is 0.18-0.19 mm, and the length of the beetle is 1.8-2.3 mm (Mahler 1988). For illustration of genitalia see Figure 7.

Geographical distribution: The species is endemic to Greenland (Mahler 1988).

Additional species

Not all specimens included in this study could be identified as belonging to one of the species listed above. When nothing else is noted, the following diagnoses and discussions are cited from the identification notes of Vladimir Gusarov and oral discussions with him.

Acrotona vagepunctata (Wollaston, 1862)

Original combination: *Homalota vagepunctata* Wollaston, 1862

Diagnosis: *Acrotona vagepunctata* (Figure 8) is described as linear, black and glossy with sparse punctation and light pubescence. The elytra are brown, convex and transversely rounded posteriorly, but not carinate. The species has a small and rounded head with slender dark-coloured antennae. The base of the antenna is brighter coloured. The legs are slender and pale red-brown. The length of the beetle is 2.1-2.6mm (Wollaston 1862, p.187).

Distribution: Wollaston (1862) reported the species to be common among *Euphorbia* plants on Lanzarote and Fuerteventura (Canary Islands). The species was later registered on two additional island, El Hierro and Tenerife (Hernández *et al.* 1994).

Discussion: In the material of this study there are two specimens similar to this species (denoted *Mocyta cf*. *vagepunctata*), but these were collected on Gran Canaria where the species is not documented.

Mocyta sp. 2 (prope *M. amblystegii*)

Diagnosis: The species is large and has large genitalia, similar to *M. amblystegii*, but the shape of the aedeagus differs.

Geographical distribution: The specimens included in this study were collected in the Canadian province of Ontario.

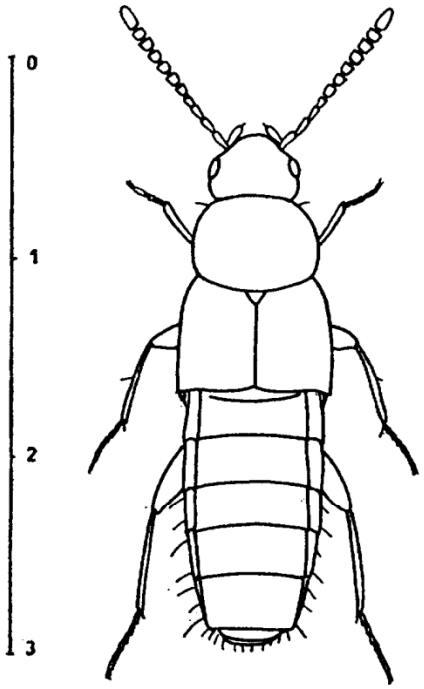
Discussion: This species does not fit any published species description that contains illustrations of genitalic characters.

Mocyta sp. 3

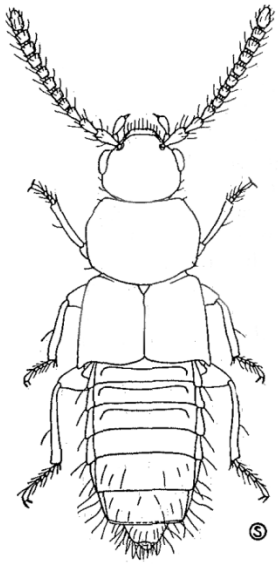
Diagnosis: The most distinct diagnostic character of this species is the presence of long umbilicus in female spermatheca. This species was illustrated and listed as *Atheta* (*Acrotona*) *sp*. by Pace (2005, fig. 22).

Geographical distribution: The specimens included in this study were collected in Greece, Israel, Turkey and Ukraine.

Discussion: This species does not fit any published species descriptions that contain illustrations of genitalic characters.



Mocyta fungi



Mocyta gilvicollis

Acrotona vagepunctata

Figure 8: Illustrations of *Mocyta fungi* by Benick & Lohse (1974, fig. 12:5), *Mocyta gilvicollis* by Scheerpeltz (1949, fig. 4) and *Acrotona vagepunctata* by Wollaston (1862, fig.Pl. VII, 8). All illustrations are scaled according to the scale (mm) of Benick & Lohse (1974).

Mocyta sp. 4 (*cf. M. clientula* sensu Benick & Lohse, 1974)

Diagnosis: The body of this species is lighter than in other species, the pronotum is brown and the elytra are yellow brown with darker area around scutellum. The legs are yellow.

Geographical distribution: The specimens included in this study were collected in Israel.

Discussion: This species does not fit any published species description that contains illustrations of genitalic characters.

Mocyta sp. 5

Diagnosis: The body of the species is very small and black. The antennae and legs are dark brown and the aedeagus is very small.

Geographical distribution: The specimen included in this study was collected in Greece (Corfu).

Discussion: This species does not fit any published species description that contains illustrations of genitalic characters.

Mocyta sp. 6

Diagnosis: The body and genitalia of the species are small. The copulatory piece in male aedeagus is bent, and the apical part of the median lobe of aedeagus is long.

Geographical distribution: The specimens included in this study were collected in Georgia, Greece, Russia (West Caucasus) and Turkey.

Discussion: This species does not fit any published species descriptions that contain illustrations of genitalic characters.

Mocyta sp. 7 (*cf. M. negligens* sensu Benick & Lohse 1974)

Diagnosis: The body and genitalia of the species are small, and the copulatory piece in male aedeagus is straight.

Geographical distribution: The specimens included in this study were collected in France (Corsica), Georgia, Italy, Russia (West Caucasus), U.K., Ukraine.

Discussion: This species does not exactly fit any published species descriptions that contain detailed illustrations of genitalic characters.

Sampling and Specimens

During the summer of 2012 sampling was done at thirty-one localities: one in Hedmark, seven in Hordaland, fourteen in Oslo, and nine in Rogaland. *Mocyta* specimens were registered at nine of these locations. In total 118 *Mocyta* specimens were collected during that year: fifty-five specimens from four localities in the Oslo area (Nøklevann, Østmarka; Ekeberg; Bøler, Østmarka; and Sognsvann, Nordmarka), forty-eight specimens from four localities in Rogaland (Sele, Klepp; Sælandsskogen, Time; Urådalen, Time; and Sandvedparken, Sandnes) and two specimens from one locality in Hordaland (Hæreid, Eidfjord). From these specimens twenty-three were selected for DNA extraction: nine from Oslo, twelve from Rogaland and one from Hordaland. In addition, one specimen of *Acrotona sylvicola* from Rogaland was selected as outgroup specimen.

Twenty-tree localities were sampled during the summer of 2013: four in Akershus, two in Hordaland, one in Oppland, ten in Oslo and six in Rogaland. The sampled material from five of these locations contained *Mocyta* specimens. The total number of collected *Mocyta* specimens this year was fourteen: one from Oslo (Ulsrud, Østmarka), two from Hordaland (Eidfjord) and eleven from three neighbouring localities in Rogaland (Sele, Klepp; Selevegen, Klepp; Selestranden, Klepp). Nine specimens were selected for DNA extraction: the specimen from Oslo, one of the specimens from Hordaland, and seven specimens from the three localities in Rogaland.

Summed, for both years, fifty-four localities were sampled, and some localities were visited both years. Fifteen of the sampled sites returned *Mocyta* specimens, in total 131 specimens, of which thirty were selected for DNA extraction.

All sampled *Mocyta* specimens from Norway were females, and only two species, *M. fungi* and *M. amplicollis*, were represented, the former being the most abundant. Both species were found in all of the three counties: Rogaland, Hordaland and Oslo. Information about the all the localities sampled can be found in Table 17 in 'Appendix 1: Specimens'.

Habitats

Table 2 and Table 3 sum up all the different types of habitats sampled during 2012 and 2013, respectively. The rows in bold types are localities where *Mocyta* specimens were found. The observed properties of the habitats are subjective - no measurements were taken. Based on the type of vegetation, orientation and exposure of the landscape, presence

of water and soil moisture assessed by hand, an overall impression of the habitat was recorded.

Table 2: Overview of types of habitat sampled in 2012, including field code, county, altitude (MASL) and observed properties of the habitat. The observed properties of the habitats are not measurements, but subjective observations. Rows highlighted with bold types are locations that returned *Mocyta* specimens.

Code	County	MASL	Habitat	Properties
EB12-31	Hedmark	324	Pine forest	dry
EB12-20	Hordaland	744	Mountain birch forest	moist
EB12-22	Hordaland	1069	Mountain plateau	dry to moist
EB12-21	Hordaland	853	Open man made space used as parking lot, gravel starting to get overgrown	dry to moist
EB12-23	**Hordaland**	**90**	**Meadow with birch, *Sorbus* and juniper**	**moist**
EB12-24	Hordaland	100	Pine forest	dry
EB12-25	Hordaland	53	Roadside meadow (hill with land slide) facing south	dry
EB12-26	Hordaland	>1	Drift kelp on coarse sandy beach by brackish water	dry to moist, salty
EB12-08	**Oslo**	**184**	**Narrow meadow at forest edge along road, under recently cut grass**	**moist**
EB12-10	**Oslo**	**267**	**Mixed forest with wet slope towards a small stream**	**moist to wet**
EB12-01	Oslo	152	Mixed forest close to lake bank, from water edge to 40 m up	moist to wet
EB12-02	Oslo	188	Mixed forest	moist
EB12-03	Oslo	147	Uncut meadow	moist
EB12-04	**Oslo**	**152**	**Mixed forest with fallen *Picea***	**moist**
EB12-05	**Oslo**	**141**	**Mixed forest**	**moist**
EB12-06	**Oslo**	**109**	**Cut meadow (hill) facing south-west surrounded by forest**	**dry**
EB12-09	Oslo	209	On *Hydnum repandum* in pine forest	moist
EB12-27	Oslo	360	Mixed forest on old rockslide, calcareous water running through ground	dry to moist
EB12-28	Oslo	384	Calcareous bog/wetland	moist to wet
EB12-29	Oslo	341	Calcareous pine forest	dry
EB12-30	Oslo	324	Calcareous grassland	dry to moist
EB12-07	Oslo	254	Stony clearing in old pine forest	dry
EB12-14	Rogaland	2	Shellsand beach with *Elymus arenarius*	dry to moist
EB12-15	Rogaland	1	Shellsand beach with *Elymus arenarius* and patches with meadow	dry to moist
EB12-13	**Rogaland**	**21**	**Meadow in garden and roadside**	**moist, salty**
EB12-19	**Rogaland**	**37**	**Roadside meadow in temperate broadleaf forest**	**moist to wet**
EB12-12	Rogaland	8	Rocky shore	moist, salty
EB12-11	Rogaland	>1	Shellsand beach	moist to wet, salty
EB12-16	**Rogaland**	**92**	**Forest of Sitka spruce**	**moist**
EB12-17	Rogaland	99	Mixed forest by small river	moist to wet
EB12-18	**Rogaland**	**109**	**Old oak forest (hill) facing west**	**moist**

Table 3: Overview of types of habitat sampled in 2013, including field code, county, altitude (MASL) and observed properties of the habitat. The observed properties of the habitats are not measurements, but subjective observations. Rows highlighted with bold types are locations that returned *Mocyta* specimens.

Code	County	MASL	Habitat	Properties
EB13-03-1	Akershus	297	Larger rock slightly inclining westward covered in lichen, mosses and grass in clearing in spruce forest	dry
EB13-03-2	Akershus	297	Moss and Ericales in clearing in spruce forest	moist
EB13-10	Akershus	284	On fresh *Lactarius deterrimus* in spruce forest	moist
EB13-11	Akershus	250	On fresh *Lactarius deterrimus* in spruce forest	moist
EB13-15A	Hordaland	0.5	Drift kelp on coarse sandy beach by brackish water	dry to moist, salty
EB13-15B	**Hordaland**	**1**	**Cut grass above coarse sandy beach by brackish water**	**dry to moist, salty**
EB13-02	Oppland	409	Spruce grove	dry to moist
EB13-01	Oslo	226	By pond in forest with old fallen pine	moist
EB13-04	Oslo	21	Ruin with leaf litter and charcoal in deciduous forest, northward slope	moist
EB13-05	Oslo	7	Ruin with leaf litter and slate chips in deciduous forest, northward slope	moist
EB13-06	Oslo	21	Deciduous forest, westward slope	dry to moist
EB13-07	Oslo	33	Exposed hill facing south, mixed shrubs	dry
EB13-08	Oslo	25	Deciduous forest with fallen, partly rotten trees	moist
EB13-09	Oslo	37	Young deciduous forest with mossy ground	dry to moist
EB13-12	Oslo	191	On rotten *Leccinum versipelle* in spruce forest	wet
EB13-13	Oslo	199	Spruce forest	moist
EB13-14	**Oslo**	**216**	**Almost dried up stream in spruce forest at edge of marshland**	**moist**
EB13-21	Rogaland	8	Old dwarf pine forest on sandy ground near beach	dry to moist, salty
EB13-20	Rogaland	5	Moss on sand dunes	dry to moist, salty
EB13-17	Rogaland	1	Two old spruce trees on sandy ground near beach	dry to moist, salty
EB13-16	**Rogaland**	**10**	**Willow and maple grove by small river**	**moist, salty**
EB13-18	**Rogaland**	**3**	**Old dwarf pine forest on sandy ground near river and beach**	**moist, salty**
EB13-19	**Rogaland**	**21**	**Compost pile in garden**	**moist, salty**

Specimens

After all the vouchers were mounted, both the newly collected specimens and the specimens from the DNA grade collection were re-identified to species by Vladimir Gusarov. A bar chart showing the number of specimens used in this study, separated into species and country, can be seen in Figure 9.

Initially, fifteen species of *Mocyta* were included in this study. Three of these were excluded for various reasons: the three specimens of *M. groenlandica* collected approximately thirty years ago, preserved in 70% ethanol at room temperature, did not yield

any PCR product; the single *M. orphana* specimen did not yield ITS2 product; and two CO1 sequences from *M. scopula* were available from a previous study (Elven *et al.* 2010), but lacked ITS2 sequences. Consequently, only thirteen of the species available were included in the analyses, to be able to compare the results provided by the two selected markers. Not all these specimens were successfully identified to species, and were denoted *Mocyta sp. 2 – 7*.

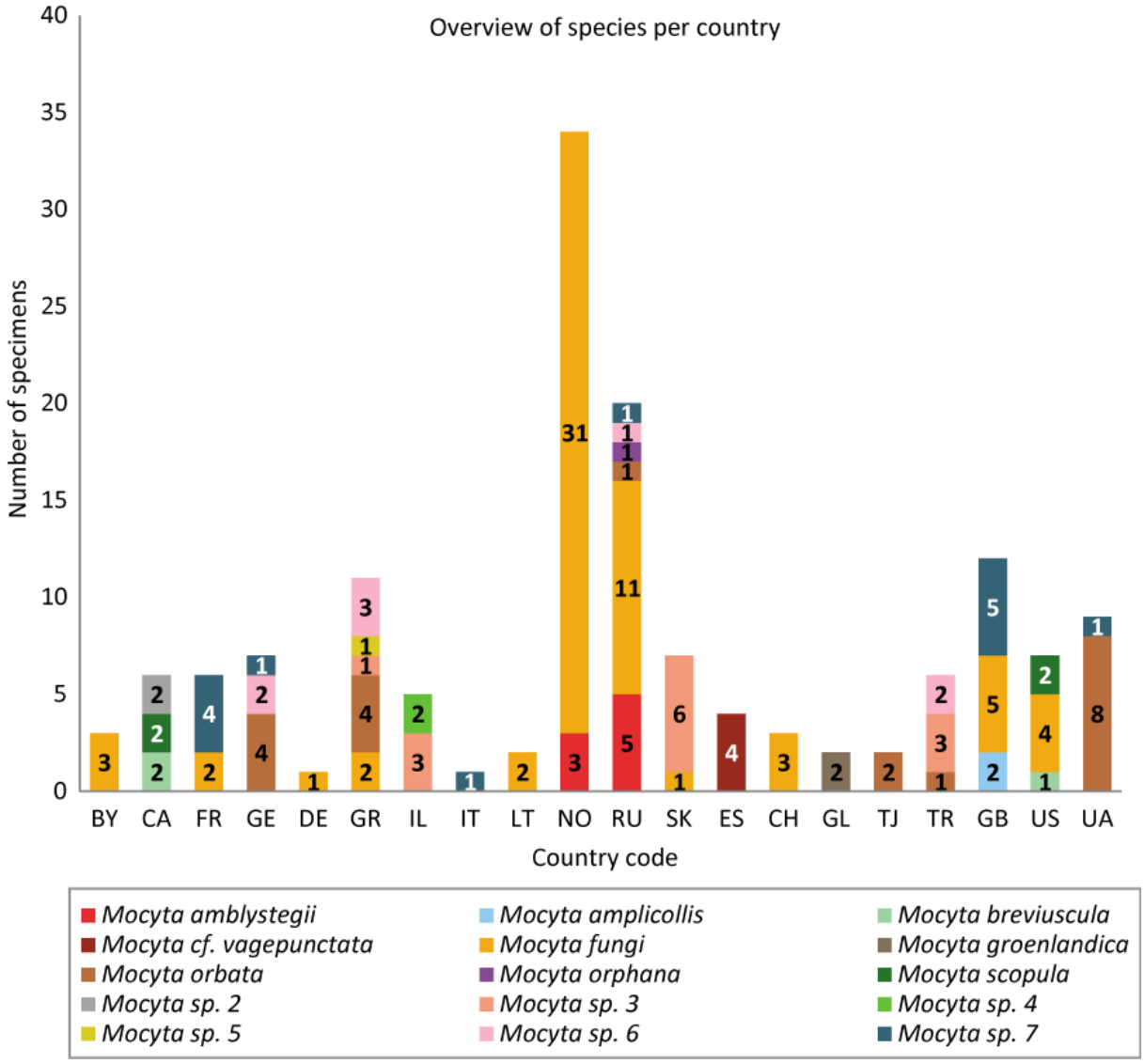


Figure 9: Bar chart giving an overview of the number of specimens selected from the museum collection (included the specimens collected during field work in 2012 and 2013), separated into species and country of origin. Total number of specimens is 157.

DNA Extraction

In total 161 specimens were used for DNA extraction, including two dry pinned *M. fungi* specimens (later excluded) from the museum collection.

Primer Testing and DNA Amplification

Eleven primer combinations (see Table 19 in 'Appendix 2: Primers') targeting the CO1 segment were tested on a batch of the DNA extracts. The three Greenland specimens did not yield any PCR product, even with the primers targeting the shortest fragments. One of the two dry pinned specimens from the museum collection did yield small amounts of PCR product, but were excluded from further analyses. The CO1 primer pair TY-J-1460 / C1-N-2416m-r worked best on the DNA extract from the *Mocyta* specimens. None of the samples tested yielded any PCR product when using the primers for ITS1, while the ITS2 primers worked well. In total, 129 samples yielded PCR product for CO1 and 151 for ITS2.

Sequencing and Alignment

From the 129 samples, 121 returned usable CO1 sequences, and 142 of the 151 returned usable ITS2 sequences. Eight of the CO1 traces and seven of the ITS2 traces were too short. One of the ITS traces had double peaks and one specimen turned out to be *Atheta* and was excluded. 111 *Mocyta* specimens yielded product for both CO1 and ITS2, and only these, in addition to two outgroup specimens, were used in the analyses.

The final length of the alignments was 860 bases for CO1 and 778 bases for ITS2.

Analyses

Model Tests

For the CO1 alignment, TIM2+I+G (transitional model, with invariable sites and gamma distributed rates among sites (Posada & Crandall 2001)) was chosen by *jModelTest 2*, both when using AIC and BIC, see Table 21 for model details. The details for the top eight models for both criteria, AIC and BIC, are available in Table 4 and Table 5, respectively.

When using AIC, *jModeltest* 2 selected TVM+I (transversial model, with invariable sites) for the ITS2 alignment, while when using BIC, TVMef+I (transversial model with equal frequencies, with invariable sites) was selected (see Table 6 and Table 7).

Table 4: Selection table from the *jModelTest* results for the CO1 alignment, sorted by AIC values. The table shows only the eight models with the lowest AIC value, 88 were tested in total. The model marked with italic types was used in the analysis in *MrBayes*.

Model	-lnL	K	AIC	delta	weight	cumWeight
TIM2+I+G	5164.148	232	10792.2961	0	0.6121	0.6121
GTR+I+G	*5162.6248*	*234*	*10793.25*	*0.9535*	*0.38*	*0.9921*
TVM+I+G	5168.0805	233	10802.1611	9.865	0.0044	0.9965
TPM2uf+I+G	5170.3184	231	10802.6368	10.3407	0.0035	1
TIM1+I+G	5177.004	232	10818.0079	25.7118	0	1
TPM1uf+I+G	5178.0815	231	10818.163	25.867	0	1
GTR+G	5181.737	233	10829.474	37.1779	0	1
HKY+I+G	5185.3731	230	10830.7462	38.4502	0	1

Table 5: Selection table from *jModelTest* results for the CO1 alignment, sorted by BIC values. The table shows only the eight models with the lowest BIC value, 88 were tested in total. The model marked with italic types was used in the analysis in *MrBayes*.

Model	-lnL	K	BIC	delta	weight	cumWeight
TIM2+I+G	5164.148	232	11895.9044	0	0.9369	0.9369
TPM2uf+I+G	5170.3184	231	11901.4882	5.5838	0.0574	0.9943
GTR+I+G	*5162.6248*	*234*	*11906.372*	*10.4674*	*0.005*	*0.9993*
TVM+I+G	5168.0805	233	11910.5263	14.6219	0.0006	1
TPM1uf+I+G	5178.0815	231	11917.0144	21.11	0	1
TIM1+I+G	5177.004	232	11921.6162	25.7118	0	1
HKY+I+G	5185.3731	230	11924.8407	28.9363	0	1
TrN+I+G	5184.9005	231	11930.6523	34.7479	0	1

Table 6: Selection table from the *jModelTest* results for the ITS2 alignment, sorted by AIC values. The table shows only the eight models with the lowest AIC value, 88 were tested in total. The model marked with italic types was used in the analysis in *MrBayes*.

Model	-lnL	K	AIC	delta	weight	cumWeight
TVM+I	2183.5012	228	4823.0023	0.0000	0.2337	0.2337
TVM+G	2183.6368	228	4823.2736	0.2713	0.2040	0.4377
GTR+I	*2183.1400*	*229*	*4824.2800*	*1.2777*	*0.1234*	*0.5611*
GTR+G	2183.2777	229	4824.5555	1.5532	0.1075	0.6686
TVM+I+G	2183.6160	229	4825.2320	2.2297	0.0766	0.7452
TVMef+I	2187.7819	225	4825.5638	2.5615	0.0649	0.8101
TVMef+G	2187.9312	225	4825.8624	2.8601	0.0559	0.8660
GTR+I+G	2183.2566	230	4826.5131	3.5108	0.0404	0.9064

Table 7: Selection table from the *jModelTest* results for the ITS2 alignment, sorted by BIC values. The table shows the eight models with the lowest AIC value, 88 were tested in total. The model marked with italic types was used in the analysis in *MrBayes*.

Model	-lnL	K	BIC	delta	weight	cumWeight
TVMef+I	2187.7819	225	5873.3273	0.0000	0.3498	0.3498
TVMef+G	2187.9312	225	5873.6259	0.2986	0.3013	0.6511
TPM3+I	2195.2982	223	5875.0463	1.7190	0.1481	0.7992
TPM3+G	2195.3786	223	5875.2073	1.8800	0.1367	0.9359
SYM+I	*2187.5106*	*226*	*5879.4414*	*6.1141*	*0.0165*	*0.9523*
SYM+G	2187.6655	226	5879.7513	6.4240	0.0141	0.9664
TVMef+I+G	2187.9114	226	5880.2429	6.9157	0.0110	0.9775
TIM3ef+I	2195.0048	224	5881.1163	7.7890	0.0071	0.9846

Maximum Likelihood

Figure 19 and Figure 20 shows ML trees for analyses based on the CO1 and ITS2 main datasets, respectively.

Bayesian Inference

The CO1 analysis ran for 11,210,000 generations. The average standard deviation of split frequencies was 0.004381, and the maximum was 0.026102. The average PSRF (Potential Scale Reduction Factor (Gelman & Rubin 1992)) for parameter values (excluding NA and >10.0) was 1.000, and maximum was 1.001.

The ITS2 analysis ran for 19,500,000 generations. The average standard deviation of split frequencies was 0.002208, and the maximum standard deviation of split frequencies was 0.010816. The average PSRF for parameter values was 1.000, and maximum was 1.000.

Comparison of Inferred Tree Topologies

Both datasets were analysed using both Bayesian Inference and Maximum Likelihood, and both the "best" models selected by BIC and AIC were run. In cases where the model selected was not available for Bayesian analyses, the best available was chosen. After the analyses, all the inferred trees based on the two markers, using different methods and models, were compared using *Compare2Trees* (Nye *et al.* 2006), see Table 8 below for results.

Table 8: Overview of the 'Overall topological score' results from comparisons of the different inferred trees using Compare2Trees. 'Topology 1' and 'Topology 2' list the two inferred trees being compared. The trees marked with bold types are discussed in detail below.

Topology 1	Topology 2	Overall topological score
CO1, MrBayes GTR+I+G	**CO1, PhyML TIM2+I+G**	**100.00 %**
ITS2, MrBayes GTR+I	ITS2, MrBayes SYM+I	100.00 %
ITS2, MrBayes GTR+I	ITS2, PhyML TVM+I	97.60 %
ITS2, MrBayes GTR+I	ITS2, PhyML TVMef+I	97.60 %
ITS2, MrBayes SYM+I	ITS2, PhyML TVM+I	97.60 %
ITS2, MrBayes SYM+I	**ITS2, PhyML TVMef+I**	**97.60 %**
ITS2, PhyML TVM+I	ITS2, PhyML TVMef+I	99.00 %

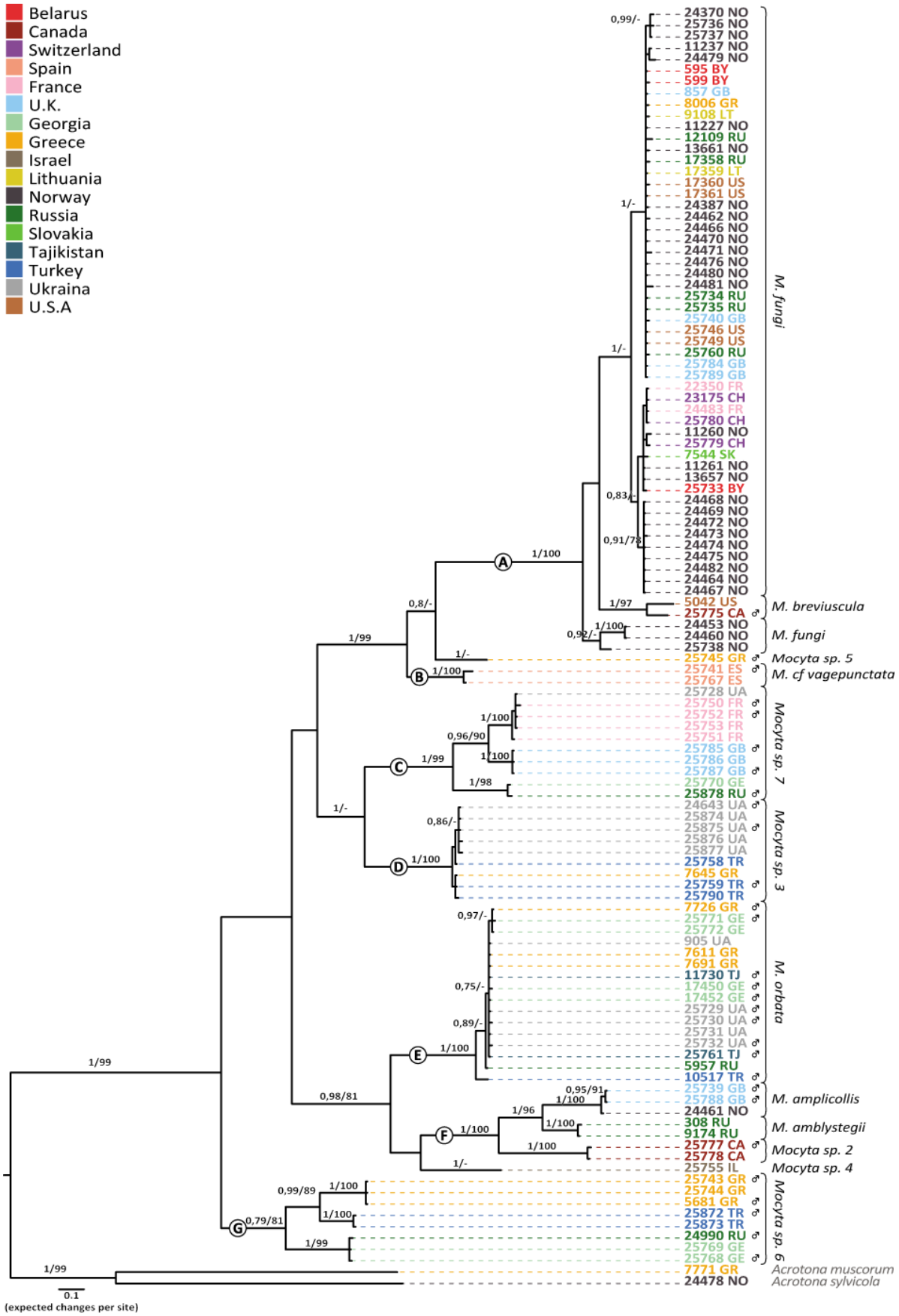


Figure 10: Tree from the Bayesian inference analysis of CO1 (GTR+I+G). The posterior probabilities are listed above branches together with the bootstrap values from the Maximum likelihood analysis (PP/BS). Selected clades are marked with encircled letters. Males are marked with sign.

Tree Topologies

In both the tree based on the CO1 alignment and the tree based on the ITS2 alignment, the bootstrap values (BS) from the Maximum likelihood (ML) tree are plotted in the tree after the posterior probabilities (PP) of the Bayesian inferred (BI) tree (see Figure 10 and Figure 11). Support values for many terminal nodes that are not discussed were omitted from the figures to improve readability. In addition, all values below 0.75 and 75 (PP and BS, respectively) were removed. Selected clades are marked in both trees, based on clustering of the sequences of the specimens.

Trees Based on the CO1 Main Dataset

The following morphospecies are included in the selected clades in the CO1 tree (Figure 10): A: *Mocyta fungi* and *M. breviuscula* (55 + 2 specimens); B: *Mocyta cf. vagepunctata* (2 specimens); C: *Mocyta sp. 7* (10 specimens); D: *Mocyta sp. 3* (9 specimens); E: *Mocyta orbata* (16 specimens); F: *Mocyta amplicollis, M. amblystegii*, *Mocyta sp. 2* and *Mocyta sp. 4* (3 + 2 + 2 + 1 specimens); and G: *Mocyta sp. 6* (8 specimens). Two *Mocyta* specimens are not included in any clade, these are 25745 GR and 25755 IL.

All *Mocyta* specimens included in the analyses form a well-supported monophyletic group (PP 1, BS 99), but the internal relationships within that group are only partially resolved. Clade A is well-supported (PP 1, BS 100), and consists of four monophyletic groups, of which only one ([5042 US and 25775 CA]) is supported by both analyses (PP 1, BS 97). The internal relationships among the four groups remain unresolved. Clade B consists of two specimens and is well-supported, and is sister to an unmarked clade consisting of Clade A and specimen 25745 GR. Clade C is well-supported (PP 1, BS 99), with the internal relationships partly resolved, suggesting two or three internal groups. The well-supported clade D (PP 1, BS 100) has little variation (sequences show differences among them at four sites). Clade E is well-supported (PP 1, BS 100), but the internal relationships have low or no support. Clade F (PP 1, BS 100) comprises two groups which are well-supported (PP 1, BS 96 and PP 1, BS 100, reading from top to bottom). Clade G is unresolved, but the internal relationships are well-supported ranging from PP 0.99 to 1 and BS 89 to 100.

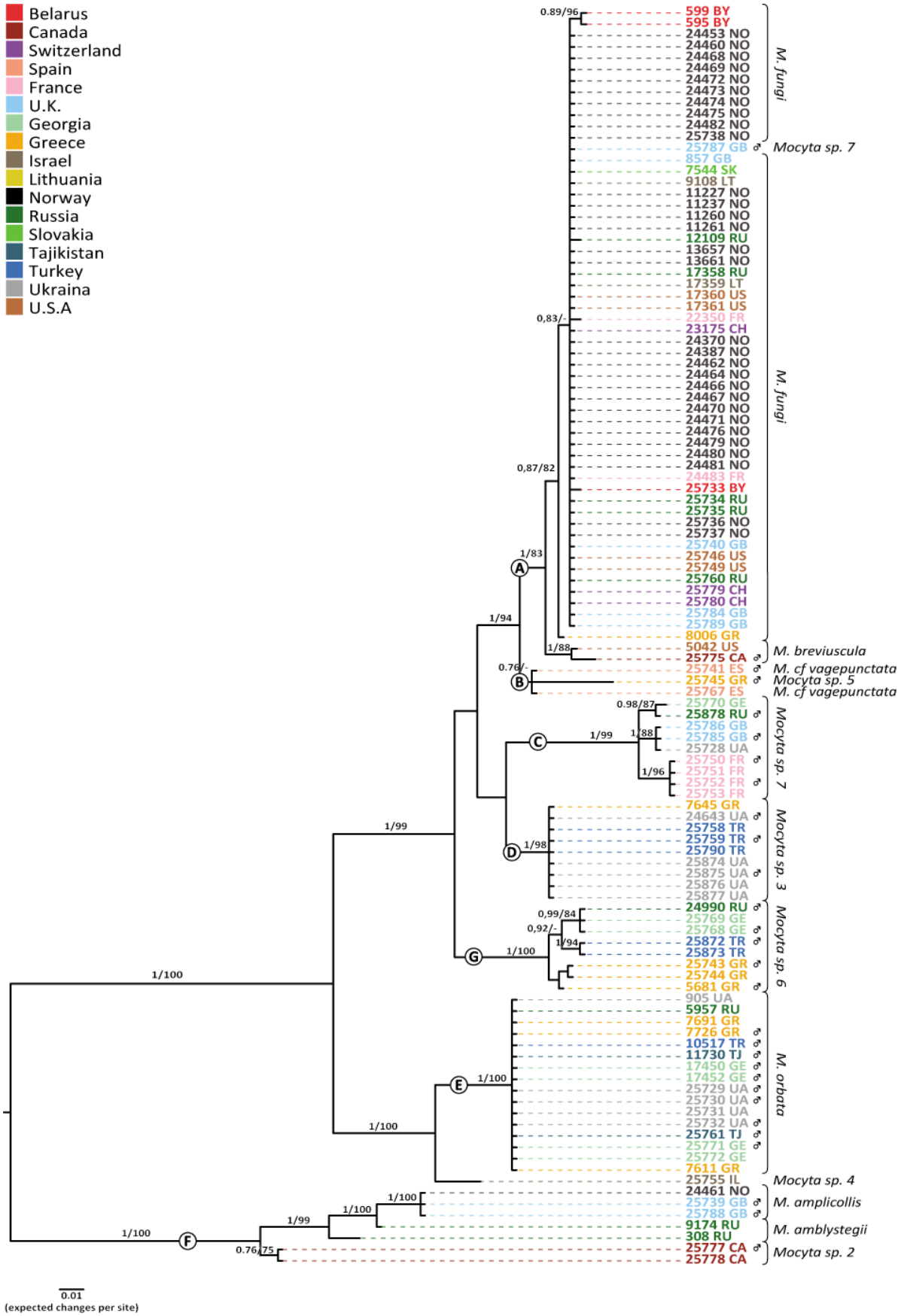


Figure 11: Tree from the Bayesian inference analysis of ITS2 (SYM+I). The posterior probabilities for the nodes are listed above branches together with the bootstrap values from the Maximum likelihood analysis (PP/BS). Selected clades are marked with encircled letters. Males are marked with sign.

Trees Based on the ITS2 Main Dataset

The following morphospecies, are included in the selected clades in the ITS2 tree (Figure 11): A: *Mocyta fungi*, *Mocyta sp. 7* and *M. breviuscula* (55 + 1 + 2 specimens); B: *Mocyta cf. vagepunctata* and *Mocyta sp. 5* (2 + 1 specimens); C: *Mocyta sp. 7* (9 specimens); D: *Mocyta sp. 3* (9 specimens); E: *Mocyta orbata* (16 specimens); F: *Mocyta amplicollis, M. amblystegii* and *Mocyta sp. 2* (3 + 2 + 2 specimens); and G: *Mocyta sp. 6* (8 specimens). One *Mocyta* specimen, 25755 IL, is not included in any clade.

Clade A is supported (PP 1, BS 83), but the internal relationships are only partly resolved. The group including sample 5042 US and 25775 CA is the only well-supported (PP 1, BS 88) internal group of clade A. Clade B is unresolved, but the node connecting clades A and B is supported (PP 1, BS 94). Clade C contains three groups, of which two are well-supported (PP 1, BS 88 and PP 1, BS 96). The sister of this clade, Clade D, is well-supported (PP 1, BS 98), and has no internal genetic variation. The internal relationship in the well-supported (PP 1, BS 100) clade G remains partly unresolved. Clade E has no internal genetic variation, is well-supported (PP 1, BS 100), and sister to 25755 IL. Clade F is sister to the rest of the specimens and is well-supported (PP 1, BS 100), but one of the first subsequent nodes has no support, leaving some of the internal relationships unresolved. All the other nodes in clade F are well-supported (PP 1 and BS 99-100).

Intra- and Interspecific Genetic Variation

Average K2P Distances

The results from the estimations in *MEGA6* showed an overall average K2P distance in the CO1 dataset of 0.0996 ± 0.0068 (0.0966 ± 0.0067 when excluding the outgroup taxa), and in the ITS2 dataset the overall distance was 0.0436 ± 0.0043. The estimated average intraspecific differences in the CO1 and the ITS2 clade datasets are shown in Table 9 and Table 10, respectively. The mean intraspecific distance was calculated across groups, and the values are 0.0199 for the groups in the CO1 clade dataset and 0.0047 in the ITS2 clade dataset. Using the 10 times mean intraspecific distance as threshold (10X threshold) to delimit species the thresholds for these datasets are 0.1986 and 0.0470, respectively.

The average difference within groups in the CO1 and ITS2 morphospecies datasets are shown in Table 11 for CO1 sequences and Table 12 for ITS2 sequences. The mean

intraspecific distance is 0.0149 for the CO1 morphospecies dataset and 0.0039 for the ITS2 morphospecies dataset, resulting in 0.149 and 0.0392 as intraspecific thresholds, respectively.

Table 9: Average K2P distances within groups of CO1 sequences, where sequences are grouped according to clades in Figure 10. The column 'Distance' shows the number of base substitutions per site from averaging over all sequence pairs within each group, and the standard deviation (SD) is also listed. At the bottom the mean intraspecific distance is calculated. 'n/c' denotes distances that could not be calculated since only one sequence was present in that group.

Group	Distance	SD
25755 IL	n/c	n/c
25745 GR	n/c	n/c
outgroup 1	n/c	n/c
outgroup 2	n/c	n/c
Clade A	0.0142	0.0022
Clade B	0.0059	0.0026
Clade C	0.0272	0.0041
Clade D	0.0020	0.0010
Clade E	0.0026	0.0007
Clade F	0.0481	0.0060
Clade G	0.0390	0.0049
Mean	**0.0199**	

Table 10: Average K2P distances within groups of ITS2 sequences, where sequences are grouped according to clades in Figure 11. The column 'Distance' shows the number of base substitutions per site from averaging over all sequence pairs within each group, and the standard deviation (SD) is also listed. At the bottom the mean intraspecific distance is calculated. 'n/c' denotes distances that could not be calculated since only one sequence was present in that group.

Group	Distance	SD
25755 IL	n/c	n/c
25745 GR	n/c	n/c
Clade A	0.0011	0.0003
Clade B	0.0000	0.0000
Clade C	0.0067	0.0022
Clade D	0.0000	0.0000
Clade E	0.0000	0.0000
Clade F	0.0206	0.0041
Clade G	0.0045	0.0018
Mean	**0.0047**	

For the last datasets, CO1 SMC and ITS2 SMC, the mean intraspecific differences are shown in Table 13 and Table 14, respectively. The mean intraspecific difference in the CO1 SMC dataset is 0.0099 and in the ITS2 SMC dataset the mean intraspecific difference is 0.0005. The respective 10X thresholds are 0.0986 and 0.0052.

The comparison of the 10X mean intraspecific differences based on the different groupings to the pairwise interspecific differences were marked using conditional formatting in MS Excel 2013. The resulting tables are in 'Appendix 4: Species Delimitation', Table 22 shows the results for CO1 and ITS2 clade dataset, Table 23 for the CO1 and ITS2 morphospecies datasets. The CO1 SMC dataset and ITS2 SMC dataset were not grouped equally, and are presented in two tables, Table 24 and Table 25, respectively.

When using the 10X threshold, only a few groups were supported as separate species in the CO1 clade dataset compared to other groups. Group '25745 GR' is separated from both 'outgroup 1' and 'outgroup 2'; '25755 IL' is only separated from 'outgroup 1'; 'Clade A' and

'Clade B' are separated from both outgroup 1 and outgroup 2; and Clade C, Clade D, Clade E and Clade F are separated from outgroup 2. Using the same threshold to delimit the species in the ITS2 clade dataset showed that Clade F is separated from all the other groups, and Clade E is separated from all but 25755 IL. The rest of the groups are clustered together in various patterns impossible to separate as congruent groups.

Table 11: Average K2P distances within groups of CO1 sequences, where sequences are grouped according to identified morphospecies. The column 'Distance' shows the number of base substitutions per site from averaging over all sequence pairs within each group, and the standard deviation (SD) is also listed. At the bottom the mean intraspecific distance is calculated. 'n/c' denotes distances that could not be calculated since only one sequence was present in that group.

Group	Distance	SD
A. muscorum	n/c	n/c
A. silvicola	n/c	n/c
Mocyta sp.4	n/c	n/c
Mocyta sp.5	n/c	n/c
M. amblystegii	0.0012	0.0012
M. amplicollis	0.0016	0.0011
M. breviuscula	0.0217	0.0051
M. cf. vagepunctata	0.0059	0.0026
M. fungi	0.0113	0.0021
M. orbata	0.0026	0.0007
Mocyta sp.2	0.0000	0.0000
Mocyta sp.3	0.0020	0.0010
Mocyta sp.6	0.0390	0.0050
Mocyta sp.7	0.0272	0.0041
Mean	**0.0149**	

Table 12: Average K2P distances within groups of ITS2 sequences, where sequences are grouped according to identified morphospecies. The column 'Distance' shows the number of base substitutions per site from averaging over all sequence pairs within each group, and the standard deviation (SD) is also listed. At the bottom the mean intraspecific distance is calculated. 'n/c' denotes distances that could not be calculated since only one sequence was present in that group.

Group	Distance	SD
Mocyta sp.4	n/c	n/c
Mocyta sp.5	n/c	n/c
M. amblystegii	0.0145	0.0044
M. amplicollis	0.0000	0.0000
M. breviuscula	0.0048	0.0026
M. cf. vagepunctata	0.0000	0.0000
M. fungi	0.0004	0.0002
M. orbata	0.0000	0.0000
Mocyta sp.2	0.0000	0.0000
Mocyta sp.3	0.0000	0.0000
Mocyta sp.6	0.0045	0.0018
Mocyta sp.7	0.0149	0.0026
Mean	**0.0039**	

In the CO1 morphospecies dataset, all the groups containing *Mocyta* specimens are delimited from the *Acrotona* outgroup taxa. The group *M.* amblystegii is separated only from *M. fungi* and *M. breviuscula*. The same is the case for *M. amplicollis*, and in addition this group is separated from *Mocyta sp. 5*. The groups *M. breviuscula* and *M. fungi* are both separated from *M. orbata*, *Mocyta sp. 2* and *Mocyta sp. 4*. In addition, *M. fungi* is separated from *Mocyta sp. 3* and *Mocyta sp. 7*. The delimitation of the other groups is, on the other hand, not supported. The groups *M. amplicollis*, *M. amblystegii* and *Mocyta sp. 2* are not delimited from each other, but from all the other groups. *Mocyta sp. 4* and *M. orbata* also

do not separate from each other, but from all the rest. The rest of the groups separate ambiguously, and do not form any congruent groups.

Table 13: Average K2P distances within groups of CO1 sequences, where sequences are grouped based on the smallest monophyletic clades that still maintained some genetic distance within groups. The column 'Distance' shows the number of base substitutions per site from averaging over all sequence pairs within each group, and the standard deviation (SD) is also listed. At the bottom the mean intraspecific distance is calculated. 'n/c' denotes distances that could not be calculated since only one sequence was present in that group.

Group	Distance	SD
A. muscorum	n/c	n/c
A. silvicola	n/c	n/c
Mocyta sp.4	n/c	n/c
Mocyta sp.5	n/c	n/c
M. amblystegii	0.0012	0.0012
M. amplicollis	0.0016	0.0011
M. breviuscula	0.0217	0.0051
M. cf. vagepunctata	0.0059	0.0026
***M. fungi* 2**	0.0081	0.0019
***M. fungi* 1**	0.0112	0.0031
M. orbata	0.0026	0.0007
Mocyta sp.2	0.0000	0.0000
Mocyta sp.3	0.0020	0.0010
***Mocyta sp.6* 2**	0.0016	0.0011
***Mocyta sp.6* 1**	0.0222	0.0040
***Mocyta sp.7* 1**	0.0359	0.0060
***Mocyta sp.7* 2**	0.0143	0.0032
Mean	**0.0099**	

Table 14: Average K2P distances within groups of ITS2 sequences, where sequences are grouped based on the smallest monophyletic clades that still maintained some genetic distance within groups. The column 'Distance' shows the number of base substitutions per site from averaging over all sequence pairs within each group, and the standard deviation (SD) is also listed. At the bottom the mean intraspecific distance is calculated. 'n/c' denotes distances that could not be calculated since only one sequence was present in that group.

Group	Distance	SD
***M. amblystegii* 1**	n/c	n/c
***M. amblystegii* 2**	n/c	n/c
Mocyta sp. 4	n/c	n/c
Mocyta sp. 5	n/c	n/c
M. amplicollis	0.0000	0.0000
M. breviuscula	0.0048	0.0026
M. cf. vagepunctata	0.0000	0.0000
***M. fungi* 7**	0.0004	0.0002
M. orbata	0.0000	0.0000
Mocyta sp. 2	0.0000	0.0000
Mocyta sp. 3	0.0000	0.0000
***Mocyta sp. 6* 3**	0.0000	0.0000
***Mocyta sp. 6* 1**	0.0000	0.0000
***Mocyta sp. 6* 2**	0.0000	0.0000
***Mocyta sp. 7* 2**	0.0000	0.0000
***Mocyta sp. 7* 1**	0.0016	0.0015
***Mocyta sp. 7* 3**	0.0000	0.0000
Mean	**0.0005**	

The CO1 SMC dataset delimits many of the groups, but not all. All the groups consisting of identified *Mocyta* specimens are separated from the two outgroup taxa. The groups *M. amblystegii* and *M. amplicollis* successfully separate from all the other groups except *Mocyta sp. 2* and each other. The group *M. breviuscula* separates from all but *M. fungi* 1 and *M. fungi* 2, and the separation of *M. fungi* 1 and *M. fungi* 2 is not supported. The group *M. cf. vagepunctata* separates from all except *Mocyta sp. 5*. The delimitation of *M. orbata* and *Mocyta sp. 4* is not supported, but *M. orbata* separates from all the other groups. *Mocyta sp. 2* is separated from all groups except *M. amblystegii*, *M. amplicollis* and *Mocyta sp. 4*. The separation of *Mocyta sp. 6* 1 and *Mocyta sp. 6* 2 is not supported, neither is the delineation of *Mocyta sp. 7* 1 and *Mocyta sp. 7* 2. *Mocyta sp. 3* as separated from all of the latter four is

not supported either. The separation of both the *Mocyta sp. 7* groups and the two *Mocyta sp. 6* groups is, however, supported by the 10X threshold.

The ITS2 SMC dataset delimits all the groups as separate species.

Species Delineation with bPTP

The estimations based on the CO1 BI tree returned between 21 and 28 species (mean number of species: 23.53) when including the outgroup taxa, and 19 to 28 species (mean number of species: 22.11) when the outgroup was excluded. The returned acceptance rate was 0.11096 for the analyses when the outgroup was included and 0.15058 when it was excluded. The simple heuristic search results for the most supported species are shown in Table 15, in total 23 species including the outgroup taxa.

The estimations based on the CO1 BI tree resulted in between 14 and 33 (mean: 20.98) species, and an acceptance rate of 0.35136. The most supported partitions (species), 19 in all, found by the simple heuristic search are shown in Table 16.

Not all the estimated species include the same samples when comparing the estimate based on the two trees. Species 10 and 14 in the CO1 tree and ITS2 tree, respectively, both include *M. amplicollis*. Species 14 (CO1 tree) and 16 (ITS2 tree) are represented by the same sample, the same is the case for Species 15 (CO1) and 17 (ITS2). The species 3, 5, 6, and 7 estimated from the CO1 dataset are equal to the species 2, 7, 5 and 1, respectively, estimated from the ITS2 dataset. These latter species are congruent with the morphospecies.

Table 15: The most supported species estimated by the bPTP service from the CO1 BI tree are numbered from 1 to 23 in the 'Species' column, the 'Support' column list the Bayesian support values after the simple heuristic search. Support values close to 1 are marked with bold types. The samples included in each estimated species are listed, and the 'Resp. Species' column show the morphospecies to which the sample numbers belong.

Species	Support	Included Samples	Resp. Species
1	**1.000**	7771GR	***Acrotona muscorum***
2	**1.000**	24478NO	***Acrotona silvicola***
3	**1.000**	25745GR	***Mocyta sp. 5***
4	0.871	25741ES, 25767ES	***M. cf. vagepunctata***
5	**0.988**	25777CA, 25778CA	***Mocyta sp. 2***
6	**1.000**	25755IL	***Mocyta sp. 4***
7	0.972	7645GR, 25759TR, 25790TR, 24643UA, 25874UA, 25875UA, 25876UA, 25877UA, 25758TR	***Mocyta sp. 3***
8	0.882	24990RU, 25769GE, 25768GE	***Mocyta sp. 6***
9	**0.989**	308RU, 9174RU	***M. amblystegii***
10	**0.986**	24461NO, 25739GB, 25788GB	***M. amplicollis***
11	**0.986**	25770GE, 25878RU	***Mocyta sp. 7***
12	0.945	25743GR, 25744GR, 5681GR	***Mocyta sp. 6***
13	**0.991**	25872TR, 25873TR	***Mocyta sp. 6***
14	**1.000**	5042US	***M. breviuscula***
15	**1.000**	25775CA	***M. breviuscula***
16	**0.996**	24453NO, 24460NO	***M. fungi***
17	**1.000**	25738NO	***M. fungi***
18	**0.992**	25728UA, 25750FR, 25752FR, 25753FR, 25751FR	***Mocyta sp. 7***
19	0.929	25785GB, 25786GB, 25787GB	***Mocyta sp. 7***
20	0.749	24468NO, 24469NO, 24472NO, 24473NO, 24474NO, 24475NO, 24482NO, 24464NO, 24467NO, 7544SK, 11260NO, 25779CH, 11261NO, 13657NO, 22350FR, 23175CH, 24483FR, 25780CH, 25733BY	***M. fungi***
21	0.809	595BY, 599BY, 857GB, 8006GR, 9108LT, 11227NO, 11237NO, 24479NO, 12109RU, 13661NO, 17358RU, 17359LT, 17360US, 17361US, 24370NO, 25736NO, 25737NO, 24387NO, 24462NO, 24466NO, 24470NO, 24471NO, 24476NO, 24480NO, 24481NO, 25734RU, 25735RU, 25740GB, 25746US, 25749US, 25760RU, 25784GB, 25789GB	***M. fungi***
22	0.881	905UA, 7611GR, 7691GR, 7726GR, 25771GE, 25772GE, 11730TJ, 17450GE, 17452GE, 25729UA, 25730UA, 25731UA, 25732UA, 25761TJ, 5957RU	***M. orbata***
23	0.888	10517TR	***M. orbata***

Table 16: The most supported species estimated by the bPTP service from the ITS2 BI tree are numbered from 1 to 23 in the 'Species' column, the 'Support' column list the Bayesian support values after the simple heuristic search. Support values close to 1 are marked with bold types. The samples included in each estimated species are listed, and the 'Resp. Species' column show the morphospecies to which the sample numbers belong.

Species	Support	Included Samples	Resp. Species
1	0.733	7645GR, 24643UA, 25758TR, 25759TR, 25790TR, 25874UA, 25875UA, 25876UA, 25877UA	***Mocyta sp. 3***
2	**1.000**	25745GR	***Mocyta sp. 5***
3	**1.000**	25767ES	***M. cf. vagepunctata***
4	**1.000**	25741ES	***M. cf. vagepunctata***
5	**1.000**	25755IL	***Mocyta sp. 4***
6	0.726	905UA, 5957RU, 7691GR, 7726GR, 10517TR, 11730TJ, 17450GE, 17452GE, 25729UA, 25730UA, 25731UA, 25732UA, 25761TJ, 25771GE, 25772GE, 7611GR	***M. orbata***
7	0.928	25777CA, 25778CA	***M. sp. 2***
8	**1.000**	308RU	***M. amblystegii***
9	0.814	25770GE, 25878RU	***Mocyta sp. 7***
10	0.798	25728UA, 25785GB, 25786GB	***Mocyta sp. 7***
11	0.751	25750FR, 25751FR, 25752FR, 25753FR	***Mocyta sp. 7***
12	0.619	599BY, 595BY, 24453NO, 24460NO, 24468NO, 24469NO, 24472NO, 24473NO, 24474NO, 24475NO, 24482NO, 25738NO, 25787GB, 857GB, 7544SK, 9108LT, 11227NO, 11237NO, 11260NO, 11261NO, 12109RU, 13657NO, 13661NO, 17358RU, 17359LT, 17360US, 17361US, 22350FR, 23175CH, 24370NO, 24387NO, 24462NO, 24464NO, 24466NO, 24467NO, 24470NO, 24471NO, 24476NO, 24479NO, 24480NO, 24481NO, 24483FR, 25733BY, 25734RU, 25735RU, 25736NO, 25737NO, 25740GB, 25746US, 25749US, 25760RU, 25779CH, 25780CH, 25784GB, 25789GB, 8006GR	***M. fungi + Mocyta sp. 7***
13	0.978	9174RU	***M. amblystegii***
14	0.790	24461NO, 25739GB, 25788GB	***M. amplicollis***
15	0.743	25743GR, 25744GR, 5681GR	***Mocyta sp. 6***
16	0.657	5042US	***M. breviuscula***
17	0.657	25775CA	***M. breviuscula***
18	0.615	24990RU, 25769GE, 25768GE	***Mocyta sp. 6***
19	0.730	25872TR, 25873TR	***Mocyta sp. 6***

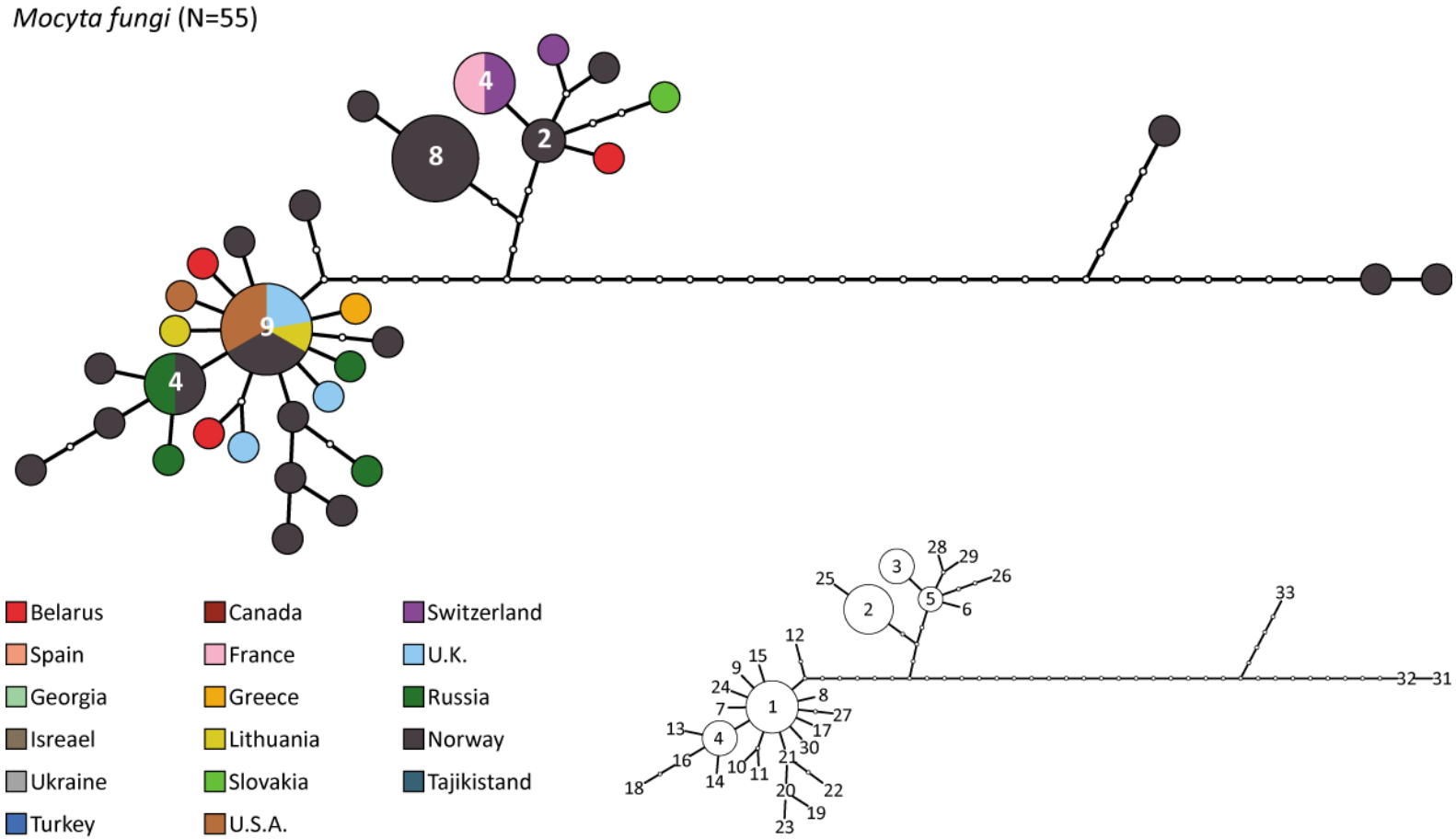


Figure 12: Haplotype network based on the CO1 sequences for species *M. fungi.* The illustration is generated by *Haploviewer* and edited manually in *Adobe Illustrator CS4*. Numbers in the pie charts represent the total number of specimens of that haplogroup; haplogroups without numbers are singletons. Smaller network shows haplotype numbers for the respective haplogroups. Colours represent the countries where the specimens were collected.

Haplotype Networks

The CO1 alignment for the *Mocyta* specimens consisted of 72 haplogroups (see for Table 26 in 'Appendix 5: Haplotypes' for details), of which 33 are represented by the 55 *M. fungi* specimens (see haplotype network in Figure 12). The haplotype network has two major clusters comprising most of the specimens, and within these clusters the haplotypes only differ by only a few mutations. The Norwegian specimens, marked with dark grey, are scattered throughout the whole network. There are three specimens separated from the rest by many mutations. These three are the same that also branch out in the inferred tree based on the CO1 alignment (see sample number 25738 NO, 24453 NO and 24460 NO in Figure 10). The haplotypes 2, 3, 5, 6, 25, 26, 28 and 29, entails specimens collected in Europe (Norway, Belarus, Slovakia, Switzerland and France). The largest cluster does not include France, Switzerland and Slovakia, but comprises a larger geographical area, covering Norway, Lithuania, Belarus, Russia, Greece, U.K. and U.S.A.

Figure 13 shows the CO1 haplotypes of *M. fungi* represented in the different counties sampled in Norway (Oslo, Rogaland and Hordaland). The *M. fungi* specimens included from Oslo represent six different haplotypes (5, 15, 18, 19, 21 and 29), of which only haplotype 5 occurs twice, and none of these are represented in other localities, neither in Norway (see Figure 13) nor in the other countries represented (see Figure 12). Haplogroup 2 consists solely of eight specimens collected in Rogaland. In total, there are nine haplogroups in smallest cluster, comprising Rogaland. Two of these (1 and 4) are widespread, but not represented in other localities in Norway. Haplotype 1, which is represented by specimens from three localities in Rogaland, is also found in specimens from Alaska, Utah and Wyoming in USA and England and Lithuania in Europe. Haplotype 4, found only at one locality in Rogaland, is the same as the one found in specimens St. Petersburg in Russia.

The ITS2 alignment consisted of 33 haplogroups (Table 26), of which 11 were represented by *M. fungi* specimens (Figure 14). Haplotype 1 is dominating, represented in 44 of the 55 specimens. Belarus is the only country not represented in this group. In total, four haplotypes are represented by specimens from Norway (see Figure 15), haplotypes 1, 4, 7 and 11. Haplotype 1 is represented by specimens from Norway (all the represented counties), Russia, Slovakia, Switzerland, France, U.K., Lithuania and U.S.A., while haplotypes 4, 7 and 11 is only represented by the Norwegian specimens.

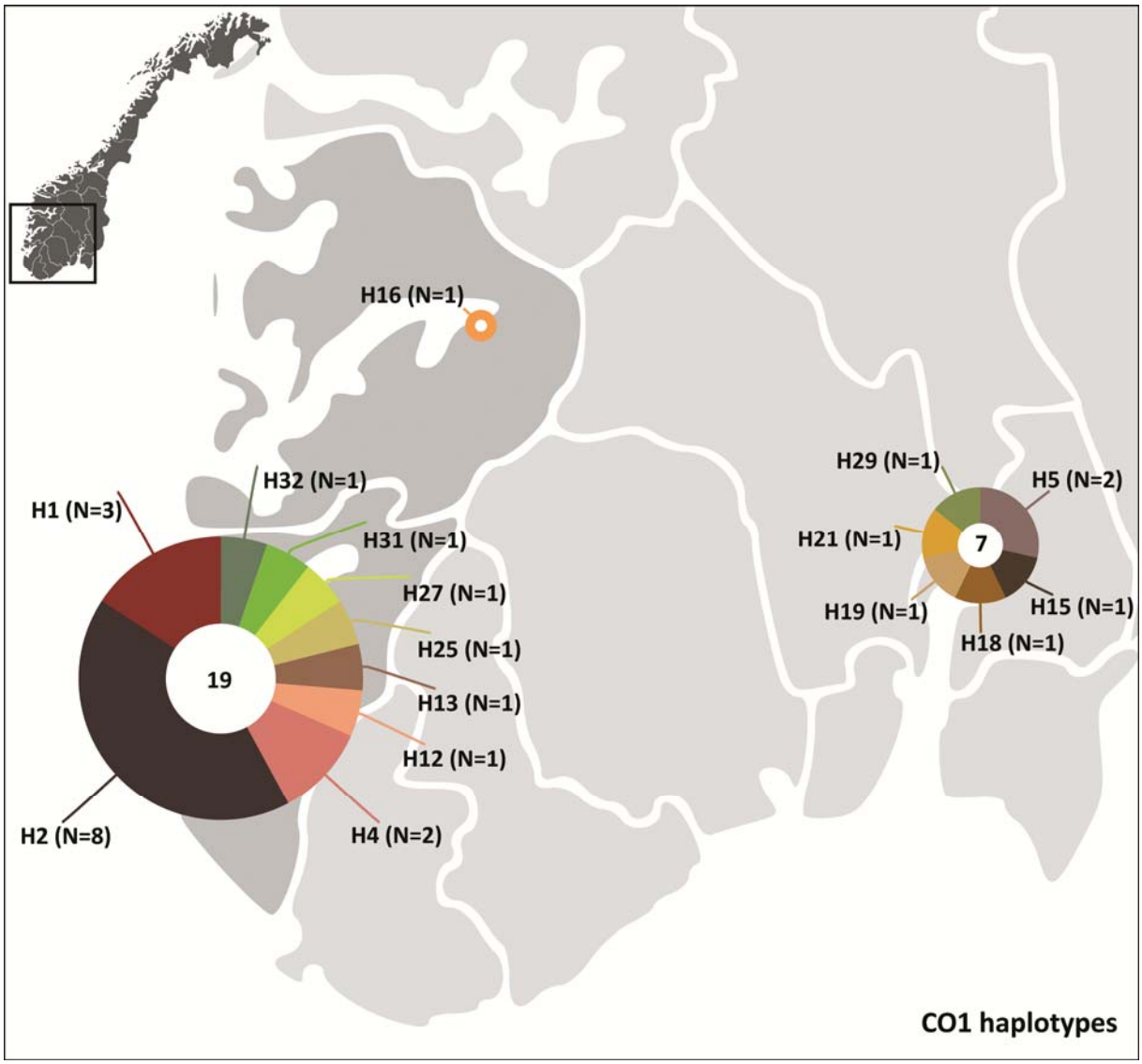


Figure 13: Map showing CO1 haplotypes, separated by different colours, of *Mocyta fungi* represented in the sampled localities in Southern Norway. Illustration made by the author, charts made with Highcharts (Highsoft AS 2014), plotted on vector map "Norway_counties_blank.svg" by Marmelad licensed under (CC BY-SA 2.5 2009).

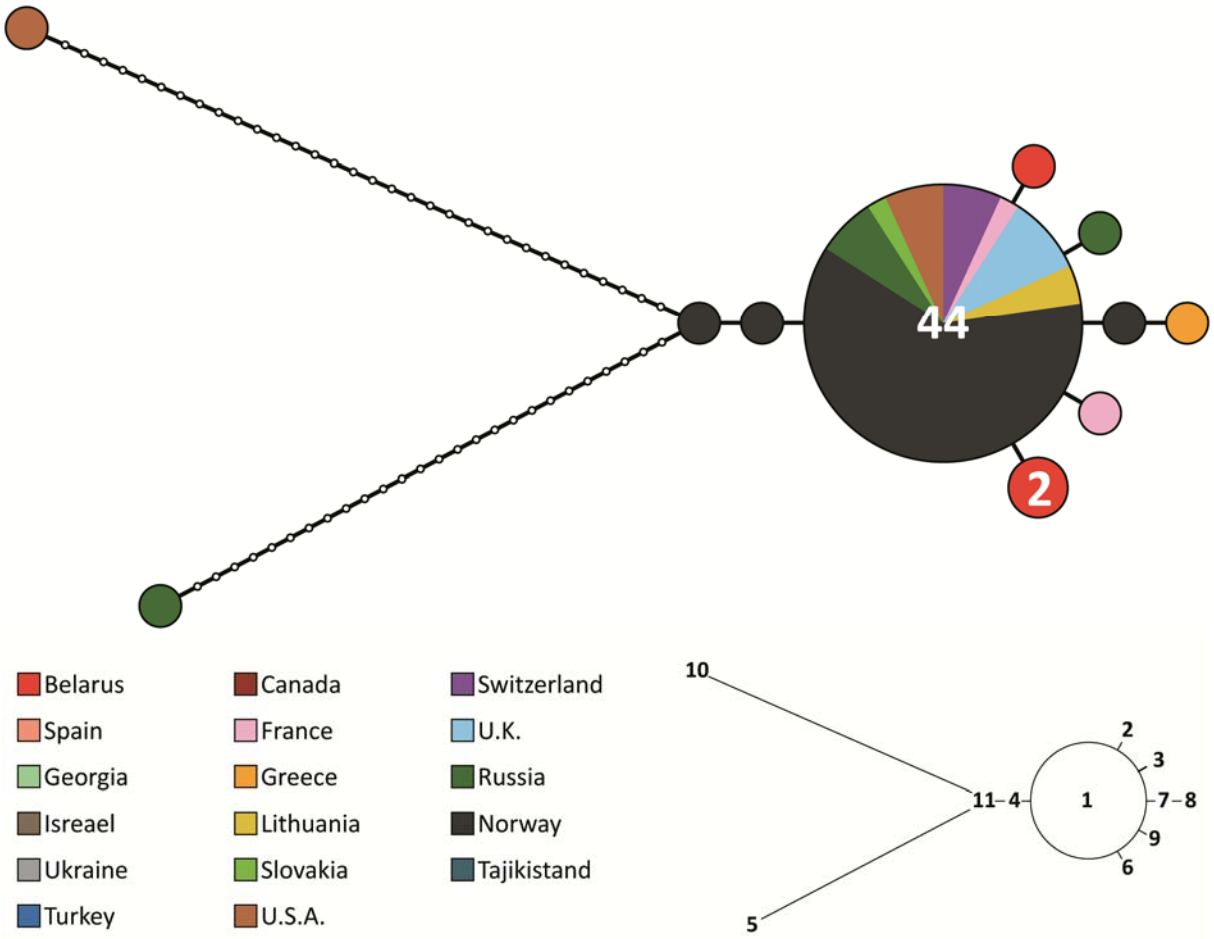


Figure 14: Haplotype network based on the ITS2 sequences for species *M. fungi.* The illustration is generated by *Haploviewer* and edited manually in *Adobe Illustrator CS4*. Numbers in the pie charts represent the total number of specimens of that haplogroup; haplogroups without numbers are singletons. Smaller network shows haplotype numbers for the respective haplogroups. Colours represent the countries where the specimens were collected.

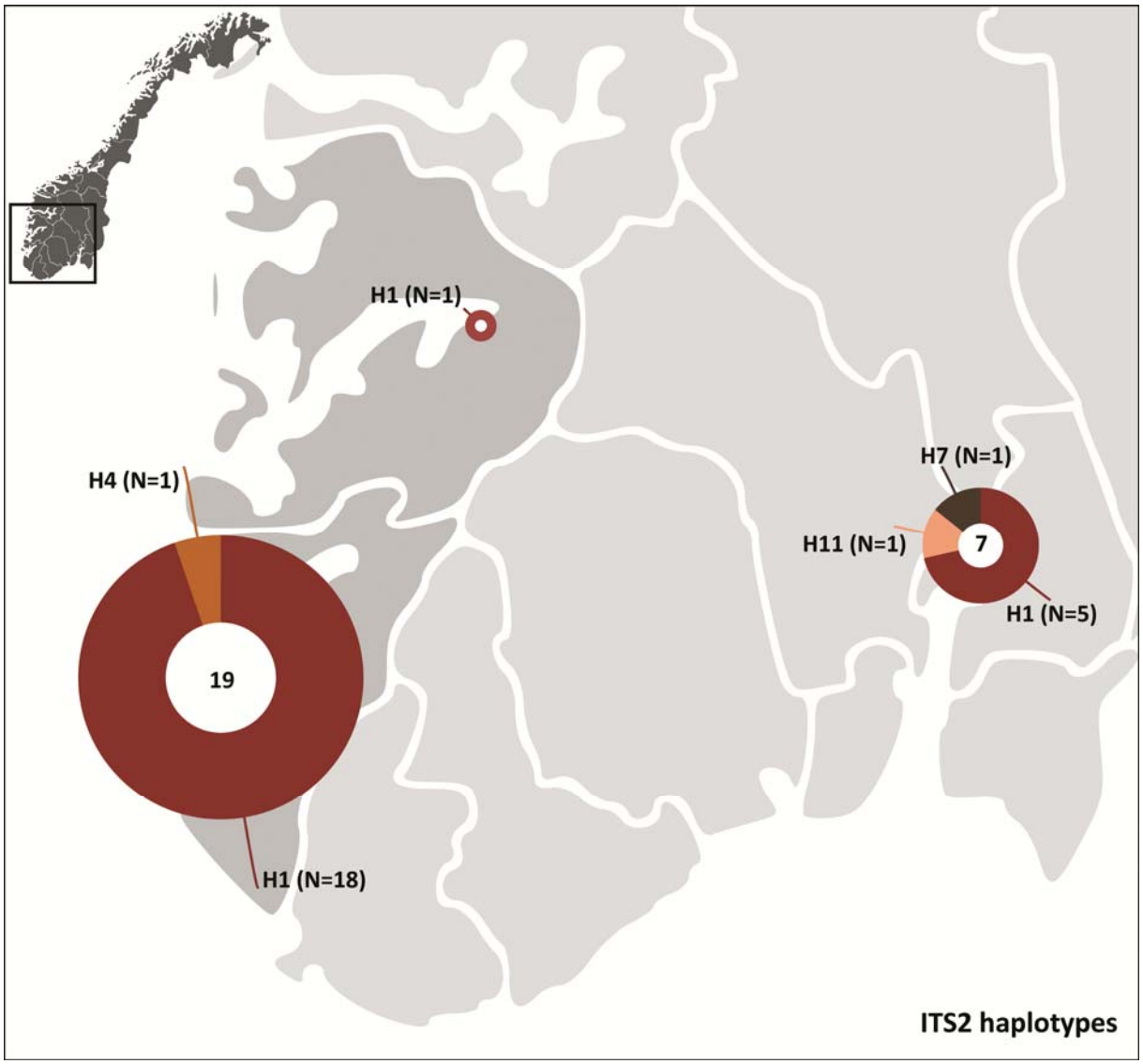


Figure 15: Map showing ITS2 haplotypes of *Mocyta fungi* represented in the sampled localities in Southern Norway. Illustration made by the author, charts made with Highcharts (Highsoft AS 2014), plotted on vector map "Norway_counties_blank.svg" by Marmelad licensed under (CC BY-SA 2.5 2009).

Discussion

Species of *Mocyta*

Investigation of the publications regarding the species of the genus *Mocyta* confirmed a lot of confusion regarding classification of these species. There are only minute morphological differences between the species, requiring in-depth knowledge and taxonomic experience to be able to differentiate between them. According to Vladimir Gusarov, the most useful characters for species identification are the genitalic characters, even for *M. fungi*.

Due to deviations of observed characters from those mentioned in available descriptions and identification keys, together with the lack of genitalic illustrations for some species, Gusarov could not identify all specimens to species level. He could however describe the morphological characters separating the unidentified species from the identified ones, and with the help of his notes and oral explanations, short diagnoses were made for each of these morphospecies.

The phylogenetic relationships among the clades formed by the *Mocyta* specimens included in this study could be resolved only in part, due to little or no statistical support for some nodes. This may in part be due to the CO1 marker evolving too fast, or not providing enough characters to resolve the relationship at the deeper nodes (the problem is less pronounced in the ITS2 marker). However, the genus *Mocyta* was confirmed to be monophyletic, as all *Mocyta* specimens formed a well-supported clade.

The included morphospecies will be discussed in detail, following the labelling of clades in the two trees based on the CO1 and ITS2 main datasets in Figure 10 and Figure 11, respectively.

Clade A

Clade A is the largest clade in these analyses, comprising all specimens identified as *M. fungi* (55 in total) together with two identified as *M. breviuscula*. *Mocyta fungi* is known to have circumpolar distribution, and has an overlapping distribution with *M. breviuscula*. All *M. fungi* specimens included in this study are females, and the only male in clade A is a Canadian *M. breviuscula*.

Clade A is well-supported in both the CO1 and ITS2 trees, but most of the internal relationships remain unresolved. Only the subclade consisting of the two *M. breviuscula* specimens is supported both by the ML and BI analyses of both markers.

The large number of *M. fungi* specimens included in this study (55 specimens), and not a single male being present among them suggests that at least the Norwegian populations sampled in 2012 and 2013 have few or no males. This may indicate that these populations are parthenogenetic. As mentioned above, the shape of the genitalia of parthenogenetic species may not be a reliable character, and for an untrained eye the spermathecae of *M. fungi* seemed to vary considerably. Morphological characters of the spermatheca of *M. fungi* vary in the specimens used in this study just as much as in "Morphologische Variabilität, Diapause und Entwicklung von *Atheta fungi* (Grav.) (Col., Staphylinidae) " by Topp (1975, fig. 4), see Figure 5. However, Vladimir Gusarov pointed out that even though the spermathecae varied, some aspects remained the same within the species: the distal part of the spermatheca has a distinct depression; the length of the umbilicus does not vary; and the thickness and total length of the proximal part are constant among individuals (see Figure 16). The total length of the proximal part of the spermatheca, as proposed by Lohse *et al.* (1990), may therefore prove to be a valid character for identification of this species.

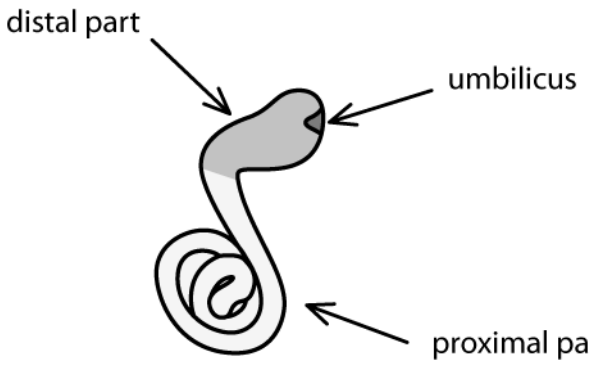


Figure 16: Illustration of the spermatheca of *Mocyta fungi*. The different parts are marked and separated by shades of grey. The shape of the spermatheca was traced by the author based on illustrations of Topp (1975, fig. 4).

Based on the analyses of the CO1 datasets the morphospecies *M. fungi* and *M. breviuscula* are not supported as separate species with respect to the intra- and interspecific variation using the 10X threshold. The clade comprising *M. fungi* and *M. breviuscula*, clade A, is only separated from the outgroup taxa in the CO1 clade dataset, and only in the CO1 SMC dataset are the two morphospecies separated from all the other groups, but not from each

other. The suggested splitting of *M. fungi* into two groups in the CO1 SMC dataset was not supported in the calculations using 10X threshold criterion. The bPTP analysis of the CO1 tree, however, estimated the *M. fungi* morphospecies to be separated into four species, but only two of these were well-supported. Based on the same analysis, the two specimens of *M. breviuscula* were estimated to be two separate and well-supported species. Calculations of the intra- and interspecific variation of the ITS2 SMC datasets supported that all the *M. fungi* specimens belong to one species, and this method also supported *M. breviuscula* being a separate species. None of the other analyses based on the ITS2 datasets supported any division of clade A.

There may be several reasons why the molecular markers used in this study do not separate the two morphospecies. First, the methods used to delimit species in this study, the 10X threshold proposed by Hebert *et al.* (2003) and the online Bayesian method bPTP by Zhang *et al.* (2013), may both be unsuitable for the genus *Mocyta*. Second, clade A may consist of only one species that is highly variable in morphological characters (i.e. *Mocyta fungi* and *M. breviuscula* are a single species). The morphological variation within clade A may just represent adaptations of different populations to different habitats and/or niches. The differences in genitalic characters, however, may mean that the two morphospecies are unable to interbreed, making them, according to the biological species concept, two sexually isolated species. If, however, some of the populations at some point became parthenogenetic and were separated by some kind of barrier, the selection on the female genitalia would be low or cease all together. This could lead to a speciation process that is not yet reflected in the molecular markers chosen for this study. It is very unlikely that these two morphospecies are one species since the genitalic characters are so different (e.g. the umbilicus of the spermatheca of *M. breviuscula* is very long, see Figure 8).

Mocyta sp. 5

The morphospecies *Mocyta sp. 5* is represented only by a single male from Greece. It does not fit to any of the available descriptions and there is a lack of matching genitalic illustrations.

In the BI and ML analyses (both markers), this specimen appeared to be closely related to clade A and B, but this relationship remains unresolved. Both the bPTP analyses estimated *Mocyta sp. 5* to be a well-supported isolated species, but using the 10X threshold method

this is only supported in the ITS2 SMC dataset. Because this morphospecies is only represented by one specimen, the intraspecific variation could not be assessed.

Clade B

Clade B consists of two specimens, one female and one male, that are morphologically very similar to *Acrotona vagepunctata* (Wollaston, 1862) and identified as *Mocyta cf. vagepunctata* in this study. These specimens were collected on Gran Canaria, while *A. vagepunctata* only has a documented distribution on El Hierro, Tenerife, Lanzarote and Fuerteventura (Wollaston 1862; Hernández *et al.* 1994). For this reason the two specimens in this study may belong to a different species. The specimens of *M. cf. vagepunctata* appear within the ingroup, close to Clade A (see Figure 10 and Figure 11), suggesting that this morphospecies should be included in the genus *Mocyta*. Delimitation of *M. cf. vagepunctata* as a separate species is not supported by the majority of the calculations using the 10X threshold criterion. Only in the ITS2 SMC dataset are these specimens separated together from the other groups, in the respective CO1 dataset these specimens are separated from all but *Mocyta sp. 5*, supporting the composition of clade B in the ITS2 tree. The dPTP analyses, however, estimated one unsupported species based on the CO1 tree, but separated this morphospecies into two well-supported species when using the ITS2 tree.

From these observations it is reasonable to suggest that *Mocyta sp. 5* and *M. cf. vagepunctata* may be closely related, if not conspecific.

Clade C

The morphospecies denoted *Mocyta sp. 7* is similar to the description of *M. negligens* by Benick and Lohse (1974), but the copulatory piece of the aedeagus is straight, which is different from the illustrations. In this study the morphospecies is represented by ten specimens (five males and five females) which form clade C (see Figure 10 and Figure 11). In the BI analysis of the CO1, this clade is sister to clade D, which consists of specimens of another morphospecies, denoted *Mocyta sp. 3*.

In both BI analyses clade C is separated into three groups, to some extent congruent with the geographic origins of the specimens. The specimens from France (Corsica) group together in both trees. The two Caucasian specimens, from Georgia and Russia (West Caucasus), also form a separate clade in both trees, confirming a geographical pattern within

this morphospecies. The remaining four specimens show a different pattern. These are three specimens from England and one from Ukraine, and the latter groups with different specimens depending on marker. In the CO1 tree it groups with the specimens from France, but in the ITS2 tree it appears together with two of the specimens from England, both well-supported. All three English specimens form a separate cluster in the CO1 tree, but in the ITS2 tree one specimen appears in clade A, together with the specimens of *M. fungi*. The molecular difference between the French and Ukrainian specimens is less than 1% (only five of 778 bases differ between them) in the ITS2 tree, but they have identical CO1 sequences. This pattern may be explained by incomplete linage sorting, where the Ukrainian specimen shares ITS2 sequences with the English specimens, while the CO1 sequences are shared between the French and Ukrainian specimens. The specimen from England appearing in clade A in the ITS2 tree is almost certainly a product of lab error (see details in the section 'Lab Error' under 'Sources of Error and Troubleshooting').

In the CO1 SMC dataset, *Mocyta sp. 7* was separated into two groups, but this was not supported by the calculations using the 10X threshold criterion. The calculations do, however, separate them both, along with *Mocyta sp. 3*, from the rest of the groups. In the corresponding ITS2 dataset, *Mocyta sp. 7* was separated into three groups, which were supported, and also separated from all the other groups. The bPTP analyses for both markers confirm the separation of the clade into three estimated species, but most of the support values are too low to be trusted.

Clade D

The genitalia of the morphospecies *Mocyta sp. 3* match an illustration in a publication by Pace (2005, fig.22), for a species listed as *Atheta* (*Acrotona*) *sp*. from Greece. One of the resembling specimens in this study is also from Greece, but from another locality, while the other specimens are from Turkey, Ukraine and Israel. Unfortunately, not all of these specimens yielded both CO1 and ITS2 sequences, resulting in the Israeli specimen being excluded. These specimens form a well-supported separate group, clade D, in the BI analyses; see Figure 10 and Figure 11. All the specimens have the same ITS2 haplotype (21), and the variation in the CO1 sequences is low (mean intraspecific distance is 0.002). In both of the bPTP analyses all specimens of *Mocyta sp. 3* group in a single species, but this estimated species has low support in CO1 and is not supported in ITS2. The 10X threshold

criterion fails to delimit clade D from the other clades, even one of the outgroup taxa, and *Mocyta sp. 3* is only separated from *M. fungi* in the ingroup when grouping is based on the recognized morphospecies. It is only separated from all the other clades in the ITS2 SMC dataset, and in the respective CO1 dataset the 10X threshold fails to separate *Mocyta sp. 6* and *Mocyta sp. 7* from *Mocyta sp. 3*.

The low intraspecific variation within both CO1 and ITS2 may indicate that this species has undergone a rapid decline in population size (due to, for example, a bottleneck effect), or that the species has had a rapid expansion of distribution (e.g. unintentional transport by humans, see section 'Geographical Patterns in *Mocyta fungi*', or natural post-glacial expansion from refugia (Elias 1994)). The distribution of specimens used in this study show a relatively low genetic diversity in the markers tested, but the distribution of sampling localities is wide-spread. All the sampled localities are close to the coast and harbour cities, which may support unintentional spread "guided" by humans.

Clade E

All the 16 specimens in this clade (ten males and six females) are identified as the morphospecies *M. orbata*. There is no variation in the ITS2 sequences, and little variation in the CO1 sequences. Two statistically unsupported species were estimated by the bPTP analyses of the CO1 tree, and one unsupported species in the ITS2 tree. The 10X threshold method delimits the specimens from all the other morphospecies in the ITS SMC dataset, but fails to separate them from *Mocyta sp. 6* and *Mocyta sp. 4* in the respective CO1 dataset.

Clade F

Three morphospecies are represented in the well-supported clade F: *M. amplicollis*, *M. amblystegii* and *Mocyta sp. 2*. This clade is also supported by the 10X threshold method based on the ITS2 datasets and the CO1 SMC dataset. The bPTP analysis based on the CO1 tree estimated three species with good support coinciding with the specimens in clade F, but analysis of the ITS2 clade dataset divided the two *M. amblystegii* specimens into two separate species.

The two specimens denoted *Mocyta sp. 2* (one male and one female) are, according to Gusarov, similar to the described species *M. amblystegii*, but the aedeagus differs in shape. This may suggest that *Mocyta sp. 2* is in fact conspecific with *M. amblystegii*, and that the

species is morphologically varied, or that this is an undescribed species, closely related to both *M. amblystegii* and *M. amplicollis*.

Mocyta sp. 4

The morphospecies denoted *Mocyta sp. 4* resembles the description of *M. clientula* by Benick and Lohse (1974), but the spermatheca and aedeagus do not exactly fit the illustrations. Unfortunately, there were no confirmed *M. clientula* specimens available for this study, meaning that there was no way to compare morphological or genetic characters of this specimen to an actual *M. clientula* specimen. In phylogenetic analyses this specimen appeared in different positions depending on the marker used, being sister to clade E in the ITS2 analyses, while in the CO1 analyses this remains unresolved.

Mocyta sp. 4 is estimated as a well-supported species in both the bPTP analyses, but is only separated from all the other groups in the ITS2 SMC dataset. The different positions of the morphospecies *Mocyta sp. 4* depending on marker may indicate incomplete linage sorting, but may also be a random effect caused by the low number of specimens represented in clade F (seven specimens identified as three different morphospecies) and *Mocyta sp. 4* only being represented by one specimen.

Clade G

The morphospecies *Mocyta sp. 6*, represented in this study by five males and three females from three geographical areas, does not exactly fit any published descriptions with illustrated genitalia, and is separated from the other specimens by several morphological characters (see '*Mocyta sp. 6*' in 'Results': 'Additional Species'. This morphospecies forms clade G, which is well-supported in the ITS2 tree, but not in the CO1 tree. The BI analyses suggest a partitioning of the specimens within this clade into three groups delimited by the geographic origin of the specimens (Greece, Turkey and Caucasus). In the analysis based on the CO1 main dataset this separation is well-supported, but the ITS2 tree fails to support this. The bPTP analyses indicate the same geographic partitioning, but the support is too low to be trusted (i.e. only one of the estimated species based on the CO1 tree is well-supported, namely the species consisting of the two Turkish specimens). In the CO1 SMC dataset *Mocyta sp. 6* is separated from all the other groups apart from *Mocyta sp. 3*, but the separation of *Mocyta sp. 6* into two groups is not supported. In the respective ITS2 dataset

there is support for *Mocyta sp. 6* as an isolated species, also when separated into several species depending on geographical origin.

Even if the support for the separation of the *Mocyta sp. 3* specimens into two groups is not well-supported, it reflects a geographical pattern within the species, implying that there is little gene flow between the populations represented in this study.

Molecular markers as a tool for species delimitation

For the most part, both the CO1 and ITS2 main dataset grouped specimens according to morphospecies, but none of the estimation methods were optimal for species delineation. The 10X threshold criterion might be too stringent, as has been the case in several other studies (Hickerson *et al.* 2006; Memon *et al.* 2006; Huang *et al.* 2008; Meier *et al.* 2008). In addition, the method is very sensitive to genera consisting of species that have different levels of variation. The 10X threshold method confirmed that all the specimens in the ingroup belong to the genus *Mocyta*, given that the selection of outgroup taxa is appropriate. Due to the problems aligning the ITS2 sequences of outgroup taxa to those of the *Mocyta* specimens, it was not possible to confirm the monophyly of *Mocyta* using this marker. Different partitioning of the datasets did, not surprisingly, dramatically alter the results of the species delimitation. When the intraspecific variation approached zero all groups separated successfully into “species”. This shows that the 10X threshold method is dependent on a high number of specimens of the same species being present in the dataset to be able to accurately delimit one species from the other, meaning that this might not be the best method for species delineation in small studies like this one.

The Bayesian based online method, bPTP, seemed more promising; it did not require prior partitioning of the dataset, and relied only on the tree resulting from other analyses. This means that no *a priori* knowledge of the specimens in the dataset is required. The bPTP method estimated a high number of species, and none of the adjustable settings in this online version seemed to be able to prevent this. The estimated species from these analyses resembled the manually chosen smallest clades in the SMC datasets.

Given that no step-by-step guide exists on how to partition a dataset containing a varying number of sequences from different species into the “correct” clades, the 10X threshold method cannot be a good replacement for traditional taxonomy. The bPTP method however,

may be a suitable for preliminary separation of specimens into species, that can eventually be checked by taxonomists.

Genetic Variation of *Mocyta fungi*

The mean KP2 distance between the specimens of the morphospecies *M. fungi* is 1.1%. This estimate may be biased because of the different number of specimens representing different parts of the world (Norway is represented by 30 specimens, Europe (including Russia, but excluding Norway) by 21 and North America by four). The mean intraspecific distance of the Norwegian specimens is 1.4%, between the European specimens the mean distance is 0.8%, while the American specimens have a mean of 0.06%. These averages seem to be correlated with the number of specimens, making any comparisons among them unreliable. The mean interspecific variation suggests that the Norwegian specimens are more closely related to the American specimens than to the European specimens, while the American and European specimens are closer related to each other than to the Norwegian specimens. Due to the suspected correlation between mean intraspecific variation and the number of included specimens, any conclusions based on these numbers were not considered trustworthy. However, if these numbers are representative of the populations sampled, this may be related to the unintentional introduction of species to other continents (see below).

Geographical Patterns in *Mocyta fungi*

Analyses of distribution of haplotypes of *M. fungi*, for both markers, showed no obvious patterns. Haplotype 1 (both for CO1 and ITS2) is widely distributed, while most of the others are restricted to specific countries.

For the CO1 haplotypes, none were shared by specimens from different counties in Norway, yet, some specimens from Rogaland shared haplotypes with specimens collected in Lithuania, U.K., U.S.A. and Russia (see Figure 12 and Figure 13). The overall genetic distance between the different haplotypes in Norway is larger than the distance between any of the haplotypes represented by other countries. This may be a reflection of the bias in the samples as discussed in the previous section, and adding more specimens from countries other than Norway might provide a different result. Examining the Norwegian specimens of *M. fungi* separately, there is no geographical pattern when comparing the genetic distance

between the haplotypes. Specimens from Oslo appear at almost all locations in the CO1 haplotype network (see haplotypes 5, 15, 18, 19, 21 and 29 in Figure 12), and the three specimens from Troms appeared at both ends of the network (haplotype 20, 23 and 33). For specimens collected in Rogaland the pattern is roughly the same, with specimens at both ends of the network. The maximum distance between the Russian specimens is six mutations, and this correlates roughly with the distribution of localities: haplotype 4 and 14 are from St. Petersburg, haplotype 17 is from Tomsk, and haplotype 22 is from the far east, Kamchatka Peninsula. When comparing with the Norwegian specimens, however, there are only two mutations separating haplotype 21 (from Oslo in Norway) from the Russian specimen from Kamchatka.

Besides Norwegian specimens, the specimens from Belarus inhabit the highest genetic distance in CO1. *Mocyta fungi* is represented by three specimens from this country, all with different CO1 haplotypes (6, 9 and 10). Between haplotype 6 and 10 there are 15 mutations, and the respective specimens are collected at different areas in Belarus, Brest and Grodno region, respectively. The last of these three haplotypes, 9, separates from haplotype 10 by three mutations but is collected in the same area.

For ITS2 there was one dominating haplotype (see Figure 14), found in 44 of the 55 specimens. Still, four haplotypes were found in the Norwegian specimens, haplotype 1, 4, 7 and 11, and three of these were singletons. Haplotype 1 was also dominating among the Norwegian specimens, but the three singletons were represented by two specimens from Oslo and one specimen from Klepp in Rogaland (see Figure 15). The dominating haplotype 1 occurred in specimens from eight different countries including Norway: Russia, Slovakia, U.S.A., Switzerland, France, U.K. and Lithuania. The specimens from Belarus do not share haplotypes with any of the specimens from other countries, and the specimen from Greece has its own type, too. Haplotype 1 is the only haplotype represented in the specimens from Great Britain, Switzerland, Slovakia and Lithuania.

Summed up, there is little evident geographic pattern in the distribution of the *M. fungi* haplotypes, even across continents. This may suggest that *M. fungi* underwent a rapid expansion relatively recently. Research confirms that many beetle species may have been unintentionally introduced to new areas during colonial times, when rocks and soil at harbours were used as ballast and thereby transported across oceans together with whatever organisms were inhabiting the soil (Lindroth 1957). Ballast was replaced with cargo

whenever needed, and soil and rocks were left at whatever harbour the boat was loaded (Lindroth 1957). These areas were often disturbed, making them uninhabitable for native species, resulting in low competition, allowing the newly arrived species populations to establish and subsequently expand (Lindroth 1957).

Geographic Restriction of Parthenogenetic Populations of *M. fungi*

As discussed in the section regarding clade A, all the specimens of *M. fungi* are females, and of the 55 specimens of *M. fungi*, 30 are from Norway. The species is also represented by specimens from nine other countries (Belarus, France, Greece, Lithuania, Russia, Slovakia, Switzerland, U.K. and U.S.A.), but the numbers of specimens from each of these other countries are low, ranging from one to five specimens. This means that it may only be a coincidence that only females are represented from the other countries, and it is impossible to conclude that the parthenogenetic populations are restricted geographically.

Ecological Preferences of *Mocyta fungi* in Norway

The sampling during the summer of 2012 and 2013 showed that the abundance of *M. fungi* was clearly higher in areas that are moister and have higher number of other invertebrates (i.e. the sampled material contained many types of invertebrates, represented by a large number of specimens, relative to sampled material from other localities). Besides that, the surrounding vegetation and type of habitat did not seem to have much effect on the presence of *M. fungi*. The CO1 haplotypes are more correlated to the localities where the specimens are collected than the ecological properties of the localities.

CO1 haplotype 2 is represented in specimens collected in Klepp and Time county in Rogaland, covering meadow at roadside, grove by small stream and forest floor in old oak forest. Several other haplotypes are represented at the same or similar habitats, e.g. haplotype 1, 4 and 19 are found in specimens collected in roadside meadows, haplotype 25 and 27 are also represented from the oak forest floor, but only haplotype 2 was found in specimens from the stream side grove.

ITS2 haplotype 1 is dominating for the Norwegian specimens, and is represented in specimens collected in all but one (EB12-04) of the listed habitats in Table 2 and Table 3.

Sources of Error and Troubleshooting

Lab Errors

Initial analyses placed four specimens in different clades in the ITS2 and CO1 trees. DNA was re-extracted from these four specimens and re-sequenced for both ITS2 and CO1 by Maria Mavrikidi to check if lab error could be responsible for this pattern. The results confirmed this suspicion. The new ITS2 sequences differed from the old, and the CO1 sequences did not, suggesting that some samples had been swapped sometime between DNA extractions and sequencing. The new (correct) ITS2 sequences replaced the old ones, the analyses were repeated and the results used in this thesis. Probably, not all the swapped samples were re-sequenced, because one specimen identified as *Mocyta sp. 7* (25787 GB) appears among specimens of *M. fungi* in the new ITS2 tree. In addition, some species have average intraspecific variation values for the ITS2 that, relative to the overall mean variation, are very high. These high values may also be due to samples being swapped in the lab.

Number of Specimens

Unfortunately, a sufficient number of specimens could not be included in this study for each species, resulting in some species not being represented in the study and some just represented by one or two specimens. This makes it impossible to confidently conclude for some of the species whether the markers delimit these species and at what threshold. The morphospecies represented by only few specimens do, however, in the BI and ML analyses of both the molecular markers, separate from the other morphospecies by several mutations. This indicates that they are separate species.

Weather and Sampling Conditions

Sampling in 2012 was mainly done in August in the Western parts of Norway, in addition to some sampling in the Oslo area in June and September. The outcome of these samplings was satisfying. Sampling in the Oslo area in 2013, however, did not yield the expected number of specimens, and the relative number of beetles found here this year was surprisingly low. The sampling methods were the same, but the extraction of invertebrates from the sampled material was mainly based on the plastic sheet method, - this may be a reason for the small number of specimens collected. Another possibility may be that the long cold winter 2012-2013 in the Southern parts of Norway, followed by a very warm and

dry July (Meteorologisk Institutt 2014) affected the survival rates of the beetles, making the available number of beetles lower. All *Mocyta* specimens found in 2013 were sampled in September, and the sampling done in August did not yield any specimens.

Conclusion

H1: The species of *Mocyta* that can be recognized based on morphology differ genetically.

The BI and ML analyses of both markers did group the different morphospecies together, but the calculations for species delineations did not result in separations that were congruent between the molecular and morphological characters, meaning that H1 must be rejected.

H2: There is, in general, significant genetic variation among different Norwegian populations, and among European populations of *Mocyta fungi.*

Due to the suspected correlation between the number of specimens represented per geographical region and the genetic variation within each of these geographical groups it was impossible to test H2 with confidence. This means that H2 can neither be accepted nor rejected.

H3: There is geographic structure in the genetic variation of *M. fungi*.

The genetic variation in *M. fungi* does not show any apparent geographic structure, but due to the low number of specimens represented from other countries than Norway it is not possible to confidently reject H3.

H4: The genetic variation of *M. fungi* corresponds to different ecological preferences.

Comparing the haplotypes of the specimens with the habitat in which the specimens were collected showed no pattern, concluding that H4 must be rejected.

H5: The parthenogenetic populations of *M. fungi* are restricted geographically.

The specimens of *M. fungi* collected and selected for this study are represented only by females. Yet, it was not possible to estimate with confidence if parthenogenetic populations were restricted geographically because of the low number of specimens represented by countries other than Norway. H5 can therefore neither be accepted nor rejected.

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Appendix 1: Specimens

Table 17: Overview of all localities sampled during summer 2012 and 2013. "Code" is a unique combination used for every collecting event, composed using the initials EB followed by year and sampling number.

Code	Label information
EB12-01	NORWAY, Oslo, 1.5 km E Bøler, Nøklevannet, 59°52.902'N 10°51.817'E WGS84, accuracy 3m, extent 30m, h=152m, forest close to lake bank, from water edge to 40 m up, *Alnus*, *Betula*, *Picea*, *Sorbus*, sifting leaf litter [EB12-01] [Garmin 60CSx] V.I.Gusarov & E.B.Josefsen 21.vi.2012
EB12-02	NORWAY, Oslo, 1.5 km E Bøler, Nøklevannet, 59°52.932'N 10°51.860'E WGS84, accuracy 6m, extent 30m, h=188m, forest with *Picea*, *Betula*, *Populus tremula*, *Oxalis*, *Vaccinium myrt*., moss, sifting leaf litter [EB12-02] [Garmin 60CSx] V.I.Gusarov & E.B.Josefsen 21.vi.2012
EB12-03	NORWAY, Oslo, Ekeberg, 59°53.508'N 10°47.158'E ± 5m, extent 10 m, h=147m, uncut meadow (*Poaceae*, *Caryophyllaceae*, *Trifolium*, *Rumex*, *Anthriscus*, *Betula* at the edge) , sifting the grass and plant litter, [EB12-03] [Garmin 60CSx] E.B.Josefsen 27.vi.2012
EB12-04	NORWAY, Oslo, Ekeberg, 59°53.543'N 10°46.242'E ± 7m WGS84, extent 10 m, h=152m, mixed forest (*Picea*, *Acer*, *Sorbus aucuparia*, *Salix*, *Corylus avellana*, *Betula*, *Equisetum*, *Oxalis acetosella*) with fallen *Picea*, sifting leaf litter, [EB12-04] [Garmin 60CSx] E.B.Josefsen 27.vi.2012
EB12-05	NORWAY, Oslo, Ekeberg, 59°53.611'N 10°46.091'N ± 10m WGS84, extent 30m, h=141m, mixed forest (*Picea*, *Acer*, *Sorbus aucuparia*, *Salix*, *Corylus avellana*, *Betula*, *Fraxinus excelsior*, *Leptosporangiatae*), sifting leaf litter, [EB12-05] [Garmin 60CSx] E.B.Josefsen 27.vi.2012
EB12-06	NORWAY, Oslo, Ekeberg, 59°53.712'N 10°45.840'E ± 15m WGS84, extent 20m, h=109m, dry, cut meadow (hill) facing south-west, surrounded by forest (*Quercus*, *Salix*, *Malus*, *Prunus*), sifting the cut grass and plant litter, [EB12-06] [Garmin 60CSx] E.B.Josefsen 27.06.2012
EB12-07	NORWAY, Oslo, Ulsrud, 59°53.822'N 10°52.216'E ± 11m WGS84, extent 0m, h=254m, stony clearing in old pine-forest (*Pinae*, *Erica*), [EB12-07] [Garmin 60CSx] E.B.Josefsen 01.vii.2012
EB12-08	NORWAY, Oslo, 1 km E Bøler, 59°52.860'N 10°51.484'E WGS84, accuracy 3m, extent 6m, h=184m, narrow meadow at forest edge along road, under recently cut grass [EB12-08] [Garmin 60CSx] V.I.Gusarov & E.B.Josefsen 21.vi.2012
EB12-09	NORWAY, Oslo, Nøklevatn, 59°52.927'N 10°52.219'E ± 18m WGS84, extent 0m, h=209m, on *Hydnum repandum* in pine Forrest, [EB12-09] [Garmin 60CSx] E.B.Josefsen 17.vii.2012
EB12-10	NORWAY, Oslo, 1 km SW Sognsvann, 59°57.968'N 10°42.472'E ± 11m WGS84, extent 30m, h=267m, mixed forest (*Picea*, *Corylus avellana*, *Fragaria vesca*) with wet slope towards a small stream, sifting leaf and plant litter, [EB12-10] [Garmin 60CSx] E.B.Josefsen & J.S.Berg 8.viii.2012
EB12-11	NORWAY, Rogaland, Sola, Ølbergstranden, 58°52.178'N 5°33.930'E ±8m WGS84, extent 5m, h=<1m, shellsand beach, sifting algae on sand, [EB12-11] [Garmin 60CSx] E.B.Josefsen 27.viii.2012
EB12-12	NORWAY, Rogaland, Sola, Vigdelsvika, 58°51.805'N 5°33.568'E ±10m WGS84, extent 10m, h=8m, rocky shore, sifting tussocks and moss, [EB12-12] [Garmin 60CSx] E.B.Josefsen 27.viii.2012
EB12-13	NORWAY, Rogaland, Klepp, Selevegen 280, 58°48.949'N 5°33.475'E ±18m WGS84, extent 30m, h=21m, meadow in garden and roadside, sifting cut grass, woodchips and moss, [EB12-13] [Garmin 60CSx] E.B.Josefsen 28.viii.2012
EB12-14	NORWAY, Rogaland, Klepp, Borestranden, Kvenhushølen, 58°48.639'N 5°32.936'E ±6m WGS84, extent 10m, h=2m, shellsand beach with *Elymus arenarius*, sifting sand and roots, [EB12-14] [Garmin 60CSx] E.B.Josefsen 28.viii.2012

Table 17 (cont.)

Code	Label information
EB12-15	NORWAY, Rogaland, Klepp, Borestranden, Kvenhushølen, 58°48.636'N 5°33.093'E ±4m WGS84, extent 5m, h=1m, shellsand beach with *Elymus arenarius* and patches with meadow, sifting sand, plants and roots, [EB12-15] [Garmin 60CSx] E.B.Josefsen 28.viii.2012
EB12-16	NORWAY, Rogaland, Time, Sælandsskogen, 58°42.649'N 5°48.099'E ±8m, extent 10m WGS84, h=92m, forest of Sitka spruce, sifting plant litter, [EB12-16] [Garmin 60CSx] E.B.Josefsen 28.viii.2012
EB12-17	NORWAY, Rogaland, Time, Sælandsskogen, 58°42.713'N 5°48.305'E ±9m WGS84, extent 2m, h=99m, mixed forest by small river, sifting moss and plant litter, [EB12-17] [Garmin 60CSx] E.B.Josefsen 28.viii.2012
EB12-18	NORWAY, Rogaland, Time, Sælandsskogen, Urådalen 58°42.717'N 5°48.388'E ±11m WGS84, extent 30m, h=109m, old oak forest (hill) facing west, sifting plant litter, [EB12-18] [Garmin 60CSx] E.B.Josefsen 28.viii.2012
EB12-19	NORWAY, Rogaland, Sandnes, Sandvedparken, 58°50.307'N 5°43.591'E ±9m WGS84, extent 1m, h=37m, roadside meadow in temperate broadleaf forest, sifting cut grass, [EB12-19] [Garmin 60CSx] E.B.Josefsen 29.viii.2012
EB12-20	NORWAY, Hordaland, Hardangervidda, Garden, 60°24.639'N 7°16.248'E ±3m WGS84, extent 20m, h=744m, birch forest (*Empetrum*, *Vaccinium*, *Calluna*, *Juniperus*, *Sorbus*, *Alnus*, *Polytrichum*, *Sphagnum*, *Leptosporangiatae*),sifting ground, [EB12-20] [Garmin 60CSx] E.B.Josefsen 30.viii.2012
EB12-21	NORWAY, Hordaland, Hardangervidda, Sysendammen, Leiro, 60°24.255'N 7°22.521'E ±28m WGS84, extent 20m, h=853m, open manmade space used as parking lot, gravel starting to get overgrown, sifting ground vegetation and gravel at the edges, [EB12-21] [Garmin 60CSx] E.B.Josefsen 30.viii.2012
EB12-22	NORWAY, Hordaland, Hardangervidda, Stora Nordmannsslepa, 60°22.913'N 7°25.053'E ±4m WGS84, extent 20m, h=1069m, mountain plateau (*Erica*, *Poaceae*, *Carex*, *Salix*, *Cladonia*),sifting ground vegetation, [EB12-22] [Garmin 60CSx] E.B.Josefsen 30.viii.2012
EB12-23	NORWAY, Hordaland, Eidfjord, Hæreid, 60°28.046'N 7°04.689'E ±11m WGS84, extent 20m, h=90m, birch, *Sorbus* and *Juniperus* forest with moss and grass ground, sifting ground vegetation, [EB12-23] [Garmin 60CSx] E.B.Josefsen 31.viii.2012
EB12-24	NORWAY, Hordaland, Eidfjord, Hæreid, 60°27.674'N 7°05.646'E ±16m WGS84, extent 1m, h=100m, pine forest, sifting woodchip pile, [EB12-24] [Garmin 60CSx] E.B.Josefsen 31.viii.2012
EB12-25	NORWAY, Hordaland, Eidfjord, Hæreid, 60°27.633'N 7°05.862'E ±22m WGS84, extent 8m, h=53m, dry roadside meadow (hill) facing south, sifting vegetation and litter, [EB12-25] [Garmin 60CSx] E.B.Josefsen & E.S.Wiborg 31.viii.2012
EB12-26	NORWAY, Hordaland, Eidfjord, Svarteholo, 60°28.745'N 7°05.554'E ±38m WGS84, extent 4m, h=0.5m, drift kelp on coarse sandy beach by brackish water, [EB12-26] [Garmin 60CSx] E.B.Josefsen & E.S.Wiborg 31.viii.2012
EB12-27	NORWAY, Oslo, Romsås, Røverkollen, 59°58.479'N 10°54.142'E ± 11m WGS84, extent 30m, h=360m, forest on old rockslide (*Betula*, *Pica*, *Alnus*, *Prunus*, *Vaccinium*, *Calluna*, *Leptosporangiatae*) calcareous water running through ground, ([EB12-27] [Garmin 60CSx] E.B.Josefsen 7.ix.2012
EB12-28	NORWAY, Oslo, Romsås, Røverkollen, 59°58.649'N 10°53.921'E ± 8m WGS84, extent 30m, h=384m, bog/wetland (*Sphagnum*, *Betula*, *Pica*, *Pinus*, *Alnus*, *Vaccinium*, *Calluna*, *Juniperus*), sifting moss and plant litter [EB12-28] [Garmin 60CSx] E.B.Josefsen & J.A.Høiby 7.ix.2012
EB12-29	NORWAY, Oslo, Romsås, Røverkollen, 59°58.435'N 10°53.952'E ± 18m WGS84, extent 30m, h=341m, dry calcareous pine forest (*Betula*, *Pinus*, *Alnus*, *Calluna*, *Juniperus*, *Sorbus*, *Poaceae*, moss, *Cladonia*), sifting lichens, moss and plant litter[EB12-29] [Garmin 60CSx] E.B.Josefsen & J.A.Høiby 7.ix.2012

Table 17 (cont.)

Code	Label information
EB12-30	NORWAY, Oslo, Romsås, Røverkollen, 59°58.386'N 10°53.967'E ± 28m WGS84, extent 30m, h=324m, dry calcareous grassland (*Betula*, *Pinus*, *Calluna*, *Juniperus*, *Geranium*, *Rubus*, *Dactylorhiza*, *Hylotelephium*, *Poaceae*, moss, lichen, *Potentilla*), sifting plant litter [EB12-30] [Garmin 60CSx] E.B.Josefsen 7.ix.2012
EB12-31	NORWAY, Hedmark, Kongsvinger, Brandval, 59°58.386'N 10°53.967'E ± 28m WGS84, extent 30m, h=324m, dry pine forest (*Pinus*, *Calluna*, *Cladonia*, *Ericaceae*), sifting lichens and plant litter [EB12-31] [Garmin 60CSx] E.B.Josefsen & E.S.Wiborg 16.ix.2012
EB13-01	NORWAY, Oslo, 1 km E Oppsal, Skøyenputten, 59°53.895'N 10°51.7044'E ±8m, extent 2m, h=226m, By pond in forest, old fallen pine, blueberry, cloudberry, spruce, pine, alder, birch, mosses, [EB13-01] [Garmin etrex] E.B.Josefsen 1.viii.2013
EB13-02	NORWAY, Oppland, Skjåk, Bismo, 61°52.7814'N 8°16.4544'E ±4m, extent 3m, h=409m, Sifting litter under spruce, [EB13-02] [Garmin etrex] E.B.Josefsen 18.viii.2013
EB13-03-1	NORWAY, Akershus, Østmarka, Nordre Elvaga, 59°52.9926'N 10°55.1826'E ±6m, extent 2m, h=297m, larger rock slightly inclining westward covered in lichen, mosses and grass in clearing in spruce forest, sifting mosses, grasses and litter [EB13-03-1] [Garmin etrex] E.B.Josefsen 24.viii.2013
EB13-03-2	NORWAY, Akershus, Østmarka, Nordre Elvaga, 59°52.9926'N 10°55.1826'E ±6m, extent 5m, h=297m, moss and *Erica* in clearing in spruce forest, sifting moss and *Erica* [EB13-03-2] [Garmin etrex] E.B.Josefsen 24.viii.2013
EB13-04	NORWAY, Oslo, Hovedøya, 59°53.8014'N 10°44.3628'E ±11m, extent 3m, h=21m, deciduous forest (*Betula*, *Salix*, *Corylus*) northward slope, ruin with leaf litter and charcoal, sifting litter [EB13-04] [Garmin etrex] E.B.Josefsen & E.S.Wiborg 25.viii.2013
EB13-05	NORWAY, Oslo, Hovedøya, 59°53.7894'N 10°44.3454'E ±11m, extent 3m, h=7m(?), deciduous forest (*Acer*, *Salix*, *Corylus*, *Fraxinus*) northward slope, ruin with leaf litter and charcoal, sifting litter [EB13-05] [Garmin etrex] E.B.Josefsen & E.S.Wiborg 25.viii.2013
EB13-06	NORWAY, Oslo, Hovedøya, 59°53.763'N 10°44.2824'E ±14m, extent 10m, h=21m(?), deciduous forest (*Corylus*, *Tilia*) westward slope, sifting litter [EB13-06] [Garmin etrex] E.B.Josefsen & E.S.Wiborg 25.viii.2013
EB13-07	NORWAY, Oslo, Hovedøya, 59°53.6964'N 10°44.4036'E ±6m, extent 2m, h=33m, Exposed hill facing south mixed shrubs (*Berberis*, *Rosa*, *Pinus*), sifting pine cones and litter (dry) [EB13-07] [Garmin etrex] E.B.Josefsen & E.S.Wiborg 25.viii.2013
EB13-08	NORWAY, Oslo, Hovedøya, 59°53.6952'N 10°44.3148'E ±7m, extent 10m, h=25m, deciduous forest (*Betula*, *Corylus*) with fallen, partly rotten trees, sifting litter [EB13-08] [Garmin etrex] E.B.Josefsen & E.S.Wiborg 25.viii.2013
EB13-09	NORWAY, Oslo, Hovedøya, 59°53.67'N 10°44.2158'E ±8m, extent 3m, h=37m, young deciduous forest (*Corylus*, *Sorbus*, *Acer*) with mossy ground, sifting litter and moss [EB13-09] [Garmin etrex] E.B.Josefsen & E.S.Wiborg 25.viii.2013
EB13-10	NORWAY, Akershus, Østmarka, Nordre Elvaga, 59°52.851'N 10°55.1592'E ±11m, extent 0m, h=284m, collecting individual specimens from *Lactarius deterrimus* in spruce forest [EB13-10] [Garmin etrex] E.B.Josefsen 24.viii.2013
EB13-11	NORWAY, Akershus, Østmarka, Nordre Elvaga, 59°52.7964'N 10°55.0842'E ±11m, extent 0m, h=250m, collecting individual specimens from *Lactarius deterrimus* in spruce forest [EB13-11] [Garmin etrex] E.B.Josefsen 24.viii.2013
EB13-12	NORWAY, Oslo, Østmarka, Nøklevann, 59°52.9728'N 10°52.5396'E ±5m, extent 0m, h=191m, collecting specimens from rotting mushroom (*Leccinum versipelle*) in spruce forest [EB13-12] [Garmin etrex] E.B.Josefsen 02.ix.2013

Table 17 (cont.)

Code	Label information
EB13-13	NORWAY, Oslo, Østmarka, Nøklevann/ Ulsrud, 59°53.2056'N 10°52.4172'E ±10m, extent 10m, h=199m, sifting litter and rotten wood in spruce forest (moist) [EB13-13] [Garmin etrex] E.B.Josefsen 02.ix.2013
EB13-14	NORWAY, Oslo, Østmarka, Ulsrud, Kattepytten, 59°53.6106'N 10°51.7494'E ±6m, extent 3m, h=216m, sifting litter and moss (*Sphagnum*) at edge of almost dry stream in spruce forest by marshland (wet) [EB13-14] [Garmin etrex] E.B.Josefsen 02.ix.2013
EB13-15A	NORWAY, Hordaland, Eidfjord 60°28.1934'N 7°04.314'E ±3m WGS84, extent 10m, h=0.5m, drift kelp on coarse sandy beach by brackish water, [EB13-15A] [Garmin etrex] E.B.Josefsen 20.ix.2013
EB13-15B	NORWAY, Hordaland, Eidfjord 60°28.1934'N 7°04.314'E ±3m WGS84, extent 10m, h=1m, cut grass above coarse sandy beach by brackish water, [EB13-15A] [Garmin etrex] E.B.Josefsen 20.ix.2013
EB13-16	NORWAY, Rogaland, Klepp, Sele 58°49.0092'N 5°33.1464'E ±3m WGS84, extent 10m, h=10m, Salix and *Acer* by small river, sifting leaf litter and moss, [EB13-16] [Garmin etrex] E.B.Josefsen 24.ix.2013
EB13-17	NORWAY, Rogaland, Klepp, Borestranden 58°48.516'N 5°33.1458'E ±3m WGS84, extent 2m, h=1m, sifting leaf litter and moss under old spruce, [EB13-17] [Garmin etrex] E.B.Josefsen 24.ix.2013
EB13-18	NORWAY, Rogaland, Klepp, Sele 58°48.7248'N 5°33.0828'E ±6m WGS84, extent 5m, h=3m, sifting grass turfs and moss under old pines on sandy ground, [EB13-18] [Garmin etrex] E.B.Josefsen 24.ix.2013
EB13-19	NORWAY, Rogaland, Klepp, Selevegen 280, 58°48.948'N 5°33.4704'E ±3m WGS84, extent 2m, h=21m, sifting cut grass, woodchips and moss in compost pile, [EB13-19] [Garmin etrex] E.B.Josefsen 24.ix.2013
EB13-20	NORWAY, Rogaland, Hå, Brusand, Vaulen 58°31.8474'N 5°46.1796'E ±4m WGS84, extent 2m, h=5m, sifting moss on sandy ground, [EB13-20] [Garmin etrex] E.B.Josefsen 25.ix.2013
EB13-21	NORWAY, Rogaland, Hå, Brusand/ Ogna 58°31.5636'N 5°46.609E ±5m WGS84, extent 10m, h=8m, sifting moss and grass under old pines on sandy ground, [EB13-20] [Garmin etrex] E.B.Josefsen 25.ix.2013

Table 18: Overview of all specimens with label information.

sample	genus	species	sex	label
271	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	RUSSIA, Magadan Reg., Severo-Evenskiy Distr., env. of Evensk [61°57'N 159°14'E], low hills surrounded by tussock (Carex, Eriophorum) tundra; in leaf litter: Alnus, Betula nana, Salix, Pinus pumila, moss. A.S.Ryabukhin…….28.vi.2007
308	*Mocyta*	*amblystegii* (Brundin, 1952)	f	RUSSIA, Magadan Reg., Severo-Evenskiy Distr., env. of Evensk [61°57'N 159°14'E], Garmanda River banks, silt and gravel, on wet soil and under gravel. A.S.Ryabukhin…….2.vii.2007
595	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	BELARUS, Grodno reg., Shchuchin distr., 5 km NNW Zachepichi, Neman Riv., riverine oak forest, 53029' 20''N 24057'52''E ±2km [WGS84; Garmin eTrex], A.Derunkov, 28.ix.2006
599	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	BELARUS, Grodno reg., Shchuchin distr., 5 km NNW Zachepichi, Neman Riv., riverine oak forest, 53029' 20''N 24057'52''E ±2km [WGS84; Garmin eTrex], A.Derunkov, 28.ix.2006
857	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	U.K., Leicestershire, Barrow on Soar, SK577167, 52.7°N 1.1°W, D.A.Lott 15.iv.2009
905	*Mocyta*	*orbata* (Erichson, 1837)	f	UKRAINE: Odessa reg., env. of Odessa, forest Luzanovsky, deciduous forest patches, leaf litter, A.Gontarenko 29.vii.2008.
907	*Mocyta*	*orbata* (Erichson, 1837)	m	UKRAINE: Odessa reg., env. of Odessa, forest Luzanovsky, deciduous forest patches, leaf litter, A.Gontarenko 29.vii.2008.
916	*Mocyta*	*orbata* (Erichson, 1837)	m	UKRAINE, Odessa reg., env. of Odessa, Svitle (Svetloye), ultra-violet light 250W, A.Gontarenko 26.vii.2008
979	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	NORWAY, Oslo, Oslo kommune, Kantarellen Terrasse, peninsula, 59º50.481'N 10º46.571'E ±6m, extent 20m, h=9m, sifting leaf litter and moss [3696] [Garmin 60CSx; WGS84] V.I.Gusarov 25.iv.2009
1000	*Oxypoda*	*brevicornis* (Stephens, 1832)	m	NORWAY, Oslo, Oslo kommune, Kantarellen Terrasse, peninsula, 59º50.481'N 10º46.571'E ±6m, extent 20m, h=9m, sifting leaf litter and moss [3696] [Garmin 60CSx; WGS84] V.I.Gusarov 25.iv.2009
1110	*Mocyta*	*orphana* (Erichson, 1837)	m	RUSSIA, St Petersburg, Pulkovo observatory park, 59º46.435'N 30º19.724'E ±6m, extent 15m, h=66m, sweeping air [3701] [Garmin 60CSx; WGS84] V.I.Gusarov 4.v.2009
3662	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	GERMANY: Mecklenburg-Vorpommern: Mecklenburg-Strelitz, Köllershof; 55°22'03,8"N 13°21'29,5"E (±140m), 100m; 16-24.v.2009; pitfall traps, 96% ethanol, leg. A.Schomann & J.Pedersen, ZMUC

Table 18 (cont.)

sample	genus	species	sex	label
4559	Acrotona	parens (Mulsant & Rey, 1852)	f	ABKHAZIA, Myusserskiy Nature Reserve, left bank of Riapshi Riv. nr mouth, N43°10'06.6'' E40°25'18.7'', h=35m, forest with Castanea, Fraxinus, Rhododendron ponticum, Laurocerasus, in leaf litter [AB-22] N. Yunakov 19.vii.2009
5042	*Mocyta*	*breviuscula* (Mäklin, 1852)	f	U.S.A., Alaska, 14 km NW Juneau, N of Hwy. 7 (Juneau Veterans Memorial Hwy.), 58º22.479'N 134º35.999'W ±7m, extent 5m, h=6m, sifting forest litter, Alnus, few Picea, Majanthemum, ferns [3839] [Garmin 60CSx; WGS84] V.I.Gusarov 4.vii.2009
5660	*Mocyta*	*laticollis* (Stephens, 1832)	f	GREECE, Corfu, env. of Agios Georgios, 39º25.444'N 19º58.956'E ±8m, h=21m, ditch bank in forest [2933] [Garmin 60CSx; WGS84] V.I.Gusarov 25.vii.2007
5681	*Mocyta*	sp. 6	m	GREECE, Corfu, env. of Agios Georgios, 39º26.070'N 19º57.263'E ±5m, h=24m, rotting watermelon and hay [2935] [Garmin 60CSx; WGS84] V.I.Gusarov 26.vii.2007
5734	*Mocyta*	*laticollis* (Stephens, 1832)	m	GREECE, Corfu, 3 km W Messogi (Mesongi), 39º28.652'N 19º54.341'E ±5m, h=15m, irrigation ditch with pool [2928] [Garmin 60CSx; WGS84] V.I.Gusarov 22.vii.2007
5957	*Mocyta*	*orbata* (Erichson, 1837)	f	RUSSIA, Krasnodar terr., Taman', B.Korotyaev 7.xi.20009
7544	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	SLOVAKIA, Jelšavský kras, Gemerskoteplická jaskyňa, 1.5 km E Jelšavská Teplica, 48°36'18"N 20°17'42"E, h=230m, forest at cave entrance, soil flotation 1-4 m from outcoming stream, 20 cm deep, [093], Gy. Makranczy 25.iv.2010
7611	*Mocyta*	*orbata* (Erichson, 1837)	f	GREECE, East Macedonia, Drama Pref., 19 km NNW Drama, Mt. Falakro, env. of Falakro Ski Resort, above parking, 41º18.054'N 24º04.216'E, accuracy 9m, extent 50m, h=1745m, alpine meadows, under stones [4360] [Garmin 60CSx; WGS84] V.I.Gusarov & J.Oßwald 23.v.2010
7645	*Mocyta*	sp. 3	f	GREECE, East Macedonia, Kavala, Pangaio, 18 km W Kavala, 5 km W Eleutheroupoli, Mt Pangeo, E slope, 40º55.174'N 24º12.021'E, accuracy 8m, extent 30m, h=612m, Fagus forest, ravine bottom, wet creek river bed, sand, stones, leaf litter [4382] [Garmin 60CSx; WGS84] V.I.Gusarov & J.Oßwald 26.v.2010
7666	*Mocyta*	*orbata* (Erichson, 1837)	f	GREECE, East Macedonia, Drama Pref., 34 km N Drama, 10 km NNE Potami, 41º28.094'N 24º09.861'E, accuracy 7m, extent 10m, h=1094m, forest with Fagus, Pinus, Picea, Betula, moss, grass, sifting leaf litter [4369] [Garmin 60CSx; WGS84] V.I.Gusarov & J.Oßwald 24.v.2010
7691	*Mocyta*	*orbata* (Erichson, 1837)	f	GREECE, East Macedonia, Drama Pref., 34 km N Drama, 10 km NNE Potami, 41º28.291'N 24º09.530'E, accuracy 9m, extent 30m, h=1102m, riverine forest with Corylus, Betula, few Alnus, sifting forest litter [4374] [Garmin 60CSx; WGS84] V.I.Gusarov & J.Oßwald 24.v.2010

Table 18 (cont.)

sample	genus	species	sex	label
7726	*Mocyta*	*orbata* (Erichson, 1837)	m	GREECE, East Macedonia, Drama Pref., 35 km N Drama, 10 km NNE Potami, 41º29.650'N 24º10.815'E, accuracy 10m, extent 50m, h=1390m, forest with *Fagus*, *Picea*, *Betula*, *Pinus*, *Vaccinium myrtillus*, grass, sifting forest litter [4376] [Garmin 60CSx; WGS84] V.I.Gusarov & J.Oßwald 24.v.2010
7771	*Acrotona*	*muscorum* (Brisout de Barneville, 1860)	f	GREECE, East Macedonia, Drama Pref., 38 km NWW Drama, 4 km W K.Vrondou, 41º16.412'N 23º43.366'E, accuracy 12m, extent 15m, h=960m, forested ravine, *Fagus*, *Alnus*, *Cornus*, *Corylus*, on rotting shoots of *Orobanche* [4351] [Garmin 60CSx; WGS84] V.I.Gusarov & J.Oßwald 22.v.2010
8006	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	GREECE, Central Macedonia, Serres Pref., 16 km NE Serres, 41º14.168-.191'N 23º40.130-.147'E, accuracy 6m, extent 5m, h=883m, river banks, *Alnus*, *Mentha* [4346] [Garmin 60CSx; WGS84] V.I.Gusarov & J.Oßwald 21.v.2010
9108	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	LITHUANIA, env. of Birštonas, 54º35.654'N 24º01.949'E, accuracy 4m, extent 4m, h=92m, field (not cultivated), in pile of last year rotten hay [4461] [Garmin 60CSx; WGS84] V.I.Gusarov 3.viii.2010
9174	*Mocyta*	*amblystegii* (Brundin, 1952)	f	RUSSIA, Primorskiy kray, Ussuriysk distr. (okrug), env. of Gorno-Tayozhnyy, 43º41.630'N 132º10.107'E ±4m, extent 20m, h=150m, broad-leaved forest, *Juglans*, *Acer*, ferns, *Equisetum*, *Carex*, on fungi [4115] [Garmin 60CSx; WGS84] V.I.Gusarov 5.ix.2009
10377	*Mocyta*	sp. 3	f	ISRAEL, Haifa, University campus, 32°45'N 35°01'E, 450m, [IL-05-06] Yu.M.Marusik, 29.xii.2010
10517	*Mocyta*	*orbata* (Erichson, 1837)	m	TURKEY, Eskişehir Prov., Çatacık Forest, 39°55'54"N 31°08'22"E, 1189m, pine stand with few oaks, [T-31], Yu.M.Marusik 27.ix.2010
10906	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	RUSSIA, 18 km S Tomsk, birch forest, "proseka", A. Babenko 13.v.2011
11197	*Mocyta*	*amplicollis* (Mulsant & Rey, 1874)	f	NORWAY, Oslo, 1 km SW Sognsvann, 59°57.968'N, 10°42.472'E ± 11m, extent 30m, h=267m, mixed forest (*Picea*, *Corylus avellana*, *Fragaria vesca*) with wet slope towards a small stream, sifting leaf and plant litter, [EB12-10] [Garmin 60CSx] E.B.Josefsen 8.viii.2012
11227	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	NORWAY, Rogaland, Sandnes, Sandvedparken, 58°50.307'N 5°43.591'E ±9m WGS84, extent 1m, h=37m, roadside meadow in temperate broadleaf forest, sifting cut grass, [EB12-19] [Garmin 60CSx] E.B.Josefsen 29.viii.2012
11237	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	NORWAY, Hordaland, Eidfjord, Hæreid, 60°28.046'N 7°04.689'E ±11m WGS84, extent 20m, h=90m, birch, *Sorbus* and juniper forest with moss and grass ground, sifting ground vegetation, [EB12-23] [Garmin 60CSx] E.B.Josefsen 31.viii.2012

Table 18 (cont.)

sample	genus	species	sex	label
11260	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	NORWAY, Oslo, 1 km SW Sognsvann, 59°57.968'N 10°42.472'E ± 11m WGS84, extent 30m, h=267m, mixed forest (*Picea*, *Corylus avellana*, *Fragaria vesca*) with wet slope towards a small stream, sifting leaf and plant litter, [EB12-10] [Garmin 60CSx] E.B.Josefsen & J.S.Berg 8.viii.2012
11261	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	NORWAY, Oslo, 1 km SW Sognsvann, 59°57.968'N 10°42.472'E ± 11m WGS84, extent 30m, h=267m, mixed forest (*Picea*, *Corylus avellana*, *Fragaria vesca*) with wet slope towards a small stream, sifting leaf and plant litter, [EB12-10] [Garmin 60CSx] E.B.Josefsen & J.S.Berg 8.viii.2012
11730	*Mocyta*	*orbata* (Erichson, 1837)	m	TAJIKISTAN, Dzhirgatal distr., 4 km W Muk vill., N slope of Peter I Mt. Range, Muksu River basin, 39°08.936'N 71°30.149'E, 2755m, ±5m, meadow, under stones and in grass, [TjN6(053)] S.Saluk 31.vii.2011
12109	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	RUSSIA, N part of Kamchatka Peninsula, Penzhyna River, env. of Kamenskoye Village, lower part of E slope by the river, 62.454°N 166.191°E, meadow in forest with *Alnus* and *Salix*, tall *Poaceae* and herbaceous vegetation, in thick layer of litter, [20] A.S. Ryabukhin 29.vii.2011
13657	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	NORWAY, Oslo, Ekeberg, 59°53.611'N 10°46.091'N ± 10m WGS84, extent 30m, h=141m, mixed forest (*Picea*, *Acer*, *Sorbus aucuparia*, *Salix*, *Corylus avellana*, *Betula*, *Fraxinus excelsior*, *Leptosporangiatae*), sifting leaf litter, [EB12-05] [Garmin 60CSx] E.B.Josefsen 27.vi.2012
13661	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	NORWAY, Oslo, Ekeberg, 59°53.712'N 10°45.840'E ± 15m WGS84, extent 20m, h=109m, dry, cut meddow (hill) facing south-west, surrounded by forest (Quercus, *Salix*, *Malus*, *Prunus*), sifting the cut grass and plant litter, [EB12-06] [Garmin 60CSx] E.B.Josefsen 27.06.2012
15467	*Mocyta*	sp. 7	m	ITALY, Lombardia, Mantua, 6 km NW Mantua, Riservo Naturale Bosco Fontana, 45º11.972'N 10º44.787'E WGS84, accuracy 3m, extent 5m, h=0m, meadows in forest, in hay pile [4947] [Garmin 60CSx] V.I.Gusarov 3.vi.2011
15784	*Mocyta*	sp. 3	m	UKRAINE, Crimea, Sudak (Sudaq) distr., Hambal Mt.R., watershed of Indol and Suuk-Su rivers, 44°56'1"N 34°52'4.9"E, h=741 m, mixed nemoral forest, sifting leaf litter in ravine under Fagus and Carpinus [CR-12-66, 176], N.N. Yunakov 6.v.2012
17356	*Acrotona*	sp. 1	f	RUSSIA, Primorskiy [Maritime] Terr., Lazo distr., env. of Lazo, Lazovskiy Nature Reserve, Lazovka River valley, 43°23'11"N 133°53'43"E, 290-310m, A.G.Koval' 13.vii.2008
17357	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	RUSSIA, St Petersburg, Pulkovo observatory park, 59º46.435'N 30º19.724'E ±6m, extent 15m, h=66m, sweeping air [3701] [Garmin 60CSx; WGS84] V.I.Gusarov 4.v.2009
17358	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	RUSSIA, St Petersburg, Pulkovo observatory park, 59º46.435'N 30º19.724'E ±6m, extent 15m, h=66m, sweeping air [3701] [Garmin 60CSx; WGS84] V.I.Gusarov 4.v.2009

Table 18 (cont.)

sample	genus	species	sex	label
17359	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	LITHUANIA, env. of Birštonas, 54º35.654'N 24º01.949'E, accuracy 4m, extent 4m, h=92m, field (not cultivated), in pile of last year rotten hay [4461] [Garmin 60CSx; WGS84] V.I.Gusarov 3.viii.2010
17360	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	U.S.A., Wyoming, Albany Co., 48km W Laramie, Medicine Nat.Forest, FR351, 41º19.114'N 106º09.728'W ±6m, h=2650m, in flood refuse near creek [2065] [Garmin eTrex; WGS84] V.I.Gusarov 26.vi.2005
17361	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	U.S.A., Wyoming, Albany Co., 48km W Laramie, Medicine Nat.Forest, FR351, 41º19.114'N 106º09.728'W ±6m, h=2650m, in flood refuse near creek [2065] [Garmin eTrex; WGS84] V.I.Gusarov 26.vi.2005
17362	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	GREECE, East Macedonia, Drama Pref., 34 km N Drama, 10 km NNE Potami, 41º28.291'N 24º09.530'E, accuracy 9m, extent 30m, h=1102m, riverine forest with *Corylus*, *Betula*, few *Alnus*, sifting forest litter [4374] [Garmin 60CSx; WGS84] V.I.Gusarov & J.Oßwald 24.v.2010
17417	*Mocyta*	*amblystegii* (Brundin, 1952)	u	RUSSIA, Chukotka Pen., Beringovskiy distr., 40 km SSW Beringovskiy, 62°43.275'N 178°55.800'E, [S-25] [17-58] A.Stekolshchikov 1.viii.2012
17418	*Mocyta*	*amblystegii* (Brundin, 1952)	f	RUSSIA, Chukotka Pen., Beringovskiy distr., 40 km SSW Beringovskiy, 62°43.275'N 178°55.800'E, [S-25] [17-58] A.Stekolshchikov 1.viii.2012
17450	*Mocyta*	*orbata* (Erichson, 1837)	m	GEORGIA, Lagodekhi Reserve, along trail to meteorological station, 41°51'38.0"N 46°20'26.5"E, 1834 m, hornbeam forest [30b], Marusik Y.M. 27.vii.2012
17452	*Mocyta*	*orbata* (Erichson, 1837)	m	GEORGIA, Lagodekhi Reserve, along trail to meteorological station, 41°51'38.0"N 46°20'26.5"E, 1834 m, hornbeam forest [30b], Marusik Y.M. 27.vii.2012
22350	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	FRANCE, Alpes Maritimes, S of Hwy M2565 - route de la Vésubie, 5 km W Saint-Martin-Vésubie, 44°4.175-.150'N 7°13.563-.583'E, accuracy 4m, extent 25m, h=1490m, forest with *Larix*, *Pinus*, *Picea*, *Abies*, moss, sifting leaf litter [F15] V.I.Gusarov 7.x.2012,
23057	*Mocyta*	sp. 7	m	U.K., London, Gunnersbury, 51.5°N 0.3°W, P.M.Hammond viii.2012
23061	*Mocyta*	sp. 7	f	U.K., Middlesex, env. of London, Chiswick House, 51°29'N 0°15'W, P.M.Hammond viii.2012
23062	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	U.K., Middlesex, env. of London, Chiswick House, 51°29'N 0°15'W, P.M.Hammond viii.2012
23175	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	SWITZERLAND, canton de Genève, 1.5 km N Dardagny, Route des Baillets, 46º12.406'N 5º59.730'E WGS84, accuracy 7m, extent 70m, h=404m, forest patch with *Quercus*, *Fraxinus*, *Carpinus betulus*, *Ficaria*, sifting leaf litter [GS-8] [Garmin 60CSx] V.I.Gusarov 11.v.2013

Table 18 (cont.)

sample	genus	species	sex	label
24370	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	NORWAY, Oslo, 1 km E Bøler, 59°52.860'N 10°51.484'E WGS84, accuracy 3m, extent 6m, h=184m, narrow meadow at forest edge along road, under recently cut grass [EB12-08] [Garmin 60CSx] V.I.Gusarov & E.B.Josefsen 21.vi.2012
24387	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	NORWAY, Oslo, Østmarka, Ulsrud, Kattepytten, 59°53.6106'N 10°51.7494'E ±6m, extent 3m, h=216m, sifting litter and moss (*Sphagnum*) at edge of almost dry stream in spruce forest by marshland (wet) [EB13-14] [Garmin etrex] E.B.Josefsen 02.ix.2013
24453	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	NORWAY, Rogaland, Klepp, Sele 58°81.208'N 5°55.138'E ±6m WGS84, extent 5m, h=3m, sifting gras turfs and moss under old pines on sandy ground, [EB13-18] [Garmin etrex] E.B.Josefsen 24.ix.2013
24460	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	NORWAY, Rogaland, Klepp, Selevegen 280, 58°48.948'N 5°33.4704'E ±3m WGS84, extent 2m, h=21m, sifting cut grass, woodchips and moss in compost pile, [EB13-19] [Garmin etrex] E.B.Josefsen 24.ix.2013
24461	*Mocyta*	*amplicollis* (Mulsant & Rey, 1874)	f	NORWAY, Rogaland, Klepp, Selevegen 280, 58°48.948'N 5°33.4704'E ±3m WGS84, extent 2m, h=21m, sifting cut grass, woodchips and moss in compost pile, [EB13-19] [Garmin etrex] E.B.Josefsen 24.ix.2013
24462	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	NORWAY, Rogaland, Klepp, Selevegen 280, 58°48.948'N 5°33.4704'E ±3m WGS84, extent 2m, h=21m, sifting cut grass, woodchips and moss in compost pile, [EB13-19] [Garmin etrex] E.B.Josefsen 24.ix.2013
24464	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	NORWAY, Rogaland, Klepp, Selevegen 280, 58°48.949'N 5°33.475'E ±18m WGS84, extent 30m, h=21m, meadow in garden and roadside, sifting cut grass, woodchips and moss, [EB12-13] [Garmin 60CSx] E.B.Josefsen 28.viii.2012
24465	*Mocyta*	*amplicollis* (Mulsant & Rey, 1874)	m	NORWAY, Hordaland, Eidfjord 60°28.1934'N 7°04.314'E ±3m WGS84, extent 10m, h=1m, cut gras above coarse sandy beach by brackish water, [EB13-15A] [Garmin etrex] E.B.Josefsen 20.ix.2013
24466	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	NORWAY, Rogaland, Klepp, Selevegen 280, 58°48.949'N 5°33.475'E ±18m WGS84, extent 30m, h=21m, meadow in garden and roadside, sifting cut grass, woodchips and moss, [EB12-13] [Garmin 60CSx] E.B.Josefsen 28.viii.2012
24467	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	NORWAY, Rogaland, Klepp, Selevegen 280, 58°48.949'N 5°33.475'E ±18m WGS84, extent 30m, h=21m, meadow in garden and roadside, sifting cut grass, woodchips and moss, [EB12-13] [Garmin 60CSx] E.B.Josefsen 28.viii.2012

Table 18 (cont.)

sample	genus	species	sex	label
24468	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	NORWAY, Rogaland, Klepp, Selevegen 280, 58°48.949'N 5°33.475'E ±18m WGS84, extent 30m, h=21m, meadow in garden and roadside, sifting cut grass, woodchips and moss, [EB12-13] [Garmin 60CSx] E.B.Josefsen 28.viii.2012
24469	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	NORWAY, Rogaland, Klepp, Selevegen 280, 58°48.949'N 5°33.475'E ±18m WGS84, extent 30m, h=21m, meadow in garden and roadside, sifting cut grass, woodchips and moss, [EB12-13] [Garmin 60CSx] E.B.Josefsen 28.viii.2012
24470	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	NORWAY, Rogaland, Klepp, Selevegen 280, 58°48.949'N 5°33.475'E ±18m WGS84, extent 30m, h=21m, meadow in garden and roadside, sifting cut grass, woodchips and moss, [EB12-13] [Garmin 60CSx] E.B.Josefsen 28.viii.2012
24471	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	NORWAY, Rogaland, Time, Sælandsskogen, Urådalen 58°42.717'N 5°48.388'E ±11m WGS84, extent 30m, h=109m, old oak forest (hill) facing west, sifting plant litter, [EB12-18] [Garmin 60CSx] E.B.Josefsen 28.viii.2012
24472	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	NORWAY, Rogaland, Time, Sælandsskogen, Urådalen 58°42.717'N 5°48.388'E ±11m WGS84, extent 30m, h=109m, old oak forest (hill) facing west, sifting plant litter, [EB12-18] [Garmin 60CSx] E.B.Josefsen 28.viii.2012
24473	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	NORWAY, Rogaland, Time, Sælandsskogen, Urådalen 58°42.717'N 5°48.388'E ±11m WGS84, extent 30m, h=109m, old oak forest (hill) facing west, sifting plant litter, [EB12-18] [Garmin 60CSx] E.B.Josefsen 28.viii.2012
24474	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	NORWAY, Rogaland, Klepp, Sele 58°81.682'N 5°55.244'E ±3m WGS84, extent 10m, h=10m, Salix and Acer by small river, sifting leaf litter and moss, [EB13-16] [Garmin etrex] E.B.Josefsen 24.ix.2013
24475	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	NORWAY, Rogaland, Klepp, Sele 58°81.682'N 5°55.244'E ±3m WGS84, extent 10m, h=10m, Salix and Acer by small river, sifting leaf litter and moss, [EB13-16] [Garmin etrex] E.B.Josefsen 24.ix.2013
24476	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	NORWAY, Rogaland, Klepp, Selevegen 280, 58°81.580'N 5°55.784'E ±3m WGS84, extent 2m, h=21m, sifting cut grass, woodchips and moss in compost pile, [EB13-19] [Garmin etrex] E.B.Josefsen 24.ix.2013
24477	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	NORWAY, Oslo, 1.5 km E Bøler, Nøklevannet, 59°52.902'N 10°51.817'E WGS84, accuracy 3m, extent 30m, h=152m, forest close to lake bank, from water edge to 40 m up, *Alnus*, *Betula*, *Picea*, *Sorbus*, sifting leaf litter [EB12-01] [Garmin 60CSx] V.I.Gusarov & E.B.Josefsen 21.vi.2012

Table 18 (cont.)

sample	genus	species	sex	label
24478	*Acrotona*	*sylvicola* (Kraatz, 1856)	f	NORWAY, Oslo, Ekeberg, 59°53.543'N 10°46.242'E ± 7m WGS84, extent 10 m, h=152m, mixed forest (*Picea*, *Acer*, *Sorbus aucuparia*, *Salix*, *Corylus avellana*, *Betula*, *Equisetum*, *Oxalis acetosella*) with fallen *Picea*, sifting leaf litter, [EB12-04] [Garmin 60CSx] E.B.Josefsen 27.vi.2012
24479	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	NORWAY, Oslo, Ekeberg, 59°53.543'N 10°46.242'E ± 7m WGS84, extent 10 m, h=152m, mixed forest (*Picea*, *Acer*, *Sorbus aucuparia*, *Salix*, *Corylus avellana*, *Betula*, *Equisetum*, *Oxalis acetosella*) with fallen *Picea*, sifting leaf litter, [EB12-04] [Garmin 60CSx] E.B.Josefsen 27.vi.2012
24480	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	NORWAY, Rogaland, Time, Sælandsskogen, 58°42.649'N 5°48.099'E ±8m, extent 10m WGS84, h=92m, forest of Sitka spruce, sifting plant litter, [EB12-16] [Garmin 60CSx] E.B.Josefsen 28.viii.2012
24481	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	NORWAY, Rogaland, Time, Sælandsskogen, 58°42.649'N 5°48.099'E ±8m, extent 10m WGS84, h=92m, forest of Sitka spruce, sifting plant litter, [EB12-16] [Garmin 60CSx] E.B.Josefsen 28.viii.2012
24482	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	NORWAY, Rogaland, Klepp, Selevegen 280, 58°48.949'N 5°33.475'E ±18m WGS84, extent 30m, h=21m, meadow in garden and roadside, sifting cut grass, woodchips and moss, [EB12-13] [Garmin 60CSx] E.B.Josefsen 28.viii.2012
24483	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	FRANCE, Alpes Maritimes, S of Hwy M2565 - route de la Vésubie, 5 km W Saint-Martin-Vésubie, 44°4.175-.150'N 7°13.563-.583'E, accuracy 4m, extent 25m, h=1490m, forest with *Larix*, *Pinus*, *Picea*, *Abies*, moss, sifting leaf litter [F15] V.I.Gusarov 7.x.2012,
24643	*Mocyta*	sp. 3	m	UKRAINE, Crimea, Yalta env., Cape Martian Nat. Res., 44°30'36.3"N 34°15'6.9"E, h=85 m, Mediterranean forest, sifting leaf litter [CR-12-30, 162], N.N. Yunakov 28.iv.2012
24990	*Mocyta*	sp. 6	m	RUSSIA, Krasnodar Terr., Adler distr., env. of Kepsha, 43º38.365'N 40º04.718'E WGS84, accuracy 9m, extent 12m, h=269m, right bank of the Kepsha river, boulders, gravel, sand, *Alnus* leaves, *Rubus* [C-86] [Garmin 60CSx] V.I.Gusarov 17.ix.2013
25726	*Acrotona*	sp. 1	f	RUSSIA, Primorskiy [Maritime] Terr., Lazo distr., Lazovskiy Nature Reserve, env. of Korpad' forest station (kordon), 43°15'50"N 134°07'56"E, 160-180m, A.G.Koval' 14.vii.2013
25727	*Mocyta*	*orbata* (Erichson, 1837)	f	UKRAINE, Odessa reg., Berezivka distr., env. of Raukhivka, deciduous forest, leaf litter, A.Gontarenko 13.x.2008
25728	*Mocyta*	sp. 7	f	UKRAINE, Odessa reg., Berezivka distr., env. of Raukhivka, deciduous forest, leaf litter, A.Gontarenko 13.x.2008
25729	*Mocyta*	*orbata* (Erichson, 1837)	m	UKRAINE, Odessa reg., Berezivka distr., env. of Raukhivka, deciduous forest, leaf litter, A.Gontarenko 13.x.2008

Table 18 (cont.)

sample	genus	species	sex	label
25730	*Mocyta*	*orbata* (Erichson, 1837)	m	UKRAINE, Odessa reg., Berezivka distr., env. of Raukhivka, deciduous forest, leaf litter, A.Gontarenko 13.x.2008
25731	*Mocyta*	*orbata* (Erichson, 1837)	f	UKRAINE, Odessa reg., Savran' distr., forest Savransky, env. of Polyanecke, deciduous forest, leaf litter, A.Gontarenko 23.vi.2008
25732	*Mocyta*	*orbata* (Erichson, 1837)	m	UKRAINE, Odessa reg., Savran' distr., forest Savransky, env. of Polyanecke, deciduous forest, leaf litter, A.Gontarenko 23.vi.2008
25733	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	BELARUS, Brest area, Bialowiezha Primeval Forest, Kamenyuki, Liatskie, pine forest, comp. 741, 52°36'19.3"N 23°47'18.7"E, A.Derunkov, 19.vi.2008
25734	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	RUSSIA, St Petersburg, Pulkovo observatory park, 59º46.435'N 30º19.724'E ±6m, extent 15m, h=66m, sweeping air [3701] [Garmin 60CSx; WGS84] V.I.Gusarov 4.v.2009
25735	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	RUSSIA, St Petersburg, Pulkovo observatory park, 59º46.435'N 30º19.724'E ±6m, extent 15m, h=66m, sweeping air [3701] [Garmin 60CSx; WGS84] V.I.Gusarov 4.v.2009
25736	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	NORWAY, Troms, Berg kommune, 3 km E Hamn, Hwy. 86, Bergsfjorden, 69º24.783'N 17º14.622'E ±4m, h=0m, sea beach [2997] [Garmin 60CSx; WGS84] V.I.Gusarov 5.viii.2007
25737	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	NORWAY, Troms, Målselv kommune, 10 km SSE Holt, Dividalen, 68º56.110'N 19º30.854'E ±4m, h=106m, in forest litter nr. River, *Betula*, *Alnus*, *Salix*, *Matteuccia*, *Huperzia*, moss [2946] [Garmin 60CSx; WGS84] V.I.Gusarov 4.viii.2007
25738	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	NORWAY, Troms, Balsfjord kommune, 8 km NNE Seljelvnes, Lakselvdalen, 69º20.724-.819'N 19º33.816-.619'E ±9m, h=243-373m, in leaf litter [2941-2942] [Garmin 60CSx; WGS84] V.I.Gusarov 3.viii.2007
25739	*Mocyta*	*amplicollis* (Mulsant & Rey, 1874)	m	U.K., Leicestershire, Loughborough Big Meadow, SK539215, pitfall traps D.A.Lott 24.iv.2009
25740	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	U.K., Leicestershire, Loughborough Big Meadow, SK539215, pitfall traps D.A.Lott 24.iv.2009
25741	*Mocyta*	cf. *vagepunctata* (Wollaston, 1862)	m	SPAIN, Canary Islands, Gran Canaria, Hwy GC-600, 6 km SW Vega de San Mateo, 27º58.097'N 15º33.954'W ±7m, extent 20m, h=1877m, pine (*Pinus canariensis*) forest and bushes (*Fabaceae*), in ant nest under stones [4277] [Garmin 60CSx; WGS84] V.I.Gusarov 6.i.2010
25742	*Mocyta*	cf. *vagepunctata* (Wollaston, 1862)	f	SPAIN, Canary Islands, Gran Canaria, Hwy GC-134, 4 km NNE San Bartolomé de Tirajana, 27º57.446'N 15º33.421'W ±3m, extent 20m, h=1849m, bushes (*Fabaceae*) and few pine (*Pinus canariensis*) trees, sifting leaf litter [4280] [Garmin 60CSx; WGS84] V.I.Gusarov 7.i.2010

Table 18 (cont.)

sample	genus	species	sex	label
25743	*Mocyta*	sp. 6	m	GREECE, Corfu, env. of Agios Georgios, 39º26.070'N 19º57.263'E ±5m, h=24m, rotting watermelon and hay [2935] [Garmin 60CSx; WGS84] V.I.Gusarov 26.vii.2007
25744	*Mocyta*	sp. 6	f	GREECE, Corfu, env. of Agios Georgios, 39º26.070'N 19º57.263'E ±5m, h=24m, rotting watermelon and hay [2935] [Garmin 60CSx; WGS84] V.I.Gusarov 26.vii.2007
25745	*Mocyta*	sp. 5	m	GREECE, Corfu, 3 km NWW Messogi (Mesongi), Mesongi River, 39º29.598'N 19º54.322'E ±8m, h=21m, river bank, sifting [2931a] [Garmin 60CSx; WGS84] V.I.Gusarov 25.vii.2007
25746	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	U.S.A., Alaska, Kenai Peninsula, Anchor Point, right bank of Anchor Point River, 59º46.353'N 151º50.145'W ±4m, extent 15m, h=10m, pebbles, sand, *Carex*, *Equisetum*, wetland [3874] [Garmin 60CSx; WGS84] V.I.Gusarov 8.vii.2009
25747	*Mocyta*	*scopula* (Casey, 1893)	m	U.S.A., Kansas, Douglas Co., 18 km SSE Lawrence, Breidenthal Preserve, 38º48.617'N 95º11.277'W ±8m, h=260m, in forest litter, *Quercus* etc. [2041] [Garmin eTrex; WGS84] V.I.Gusarov 18.vi.2005
25748	*Mocyta*	*scopula* (Casey, 1893)	f	U.S.A., Kansas, Douglas Co., 18 km SSE Lawrence, Breidenthal Preserve, 38º48.617'N 95º11.277'W ±8m, h=260m, in forest litter, *Quercus* etc. [2041] [Garmin eTrex; WGS84] V.I.Gusarov 18.vi.2005
25749	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	U.S.A., Utah, Summit Co., 15 km NW Kamas, Rockport Res., 40º45.275'N 111º22.537'W ±5m, h=1870m, lake and reservoir banks, in flood refuse and material from rodent burrow [2079-2080] [Garmin eTrex; WGS84] V.I.Gusarov 28.vi.2005
25750	*Mocyta*	sp. 7	m	FRANCE, Corse, 16.4 km NEE Tiuccia, 7 km E Lopigna, SE of Route D4, a creek in the u Cruzini Riv. basin, 42º06.328'N 8º55.716'E, accuracy 7m, extent 20m, h=280m, river banks, stones, gravel, moss, *Buxus* along creek, flooding banks [4404] [Garmin 60CSx; WGS84] V.I.Gusarov 15.vii.2010
25751	*Mocyta*	sp. 7	f	FRANCE, Corse, 16.4 km NEE Tiuccia, 7 km E Lopigna, SE of Route D4, a creek in the u Cruzini Riv. basin, 42º06.328'N 8º55.716'E, accuracy 7m, extent 20m, h=280m, river banks, stones, gravel, moss, *Buxus* along creek, flooding banks [4404] [Garmin 60CSx; WGS84] V.I.Gusarov 15.vii.2010
25752	*Mocyta*	sp. 7	m	FRANCE, Corse, 15.6 km NEE Tiuccia, 6.3 km E Lopigna, S of Route D125, u Cruzini Riv. valley, 42º06.332'N 8º55.134'E WGS84, accuracy 10m, extent 20m, h=237m, creek banks and waterfall, in wet moss and humid leaf litter close to creek [4403] [Garmin 60CSx] V.I.Gusarov 15.vii.2010
25753	*Mocyta*	sp. 7	f	FRANCE, Corse, 15.6 km NEE Tiuccia, 6.3 km E Lopigna, S of Route D125, u Cruzini Riv. valley, 42º06.332'N 8º55.134'E WGS84, accuracy 10m, extent 20m, h=237m, creek banks and waterfall, in wet moss and humid leaf litter close to creek [4403] [Garmin 60CSx] V.I.Gusarov 15.vii.2010
25754	*Mocyta*	sp. 4 cf. *M. clientula* sensu Benick	m	ISRAEL, Judean Hills, 1 km E Beit Shemesh, 31°44'N 35°00'E, 230m, [IL-12] Yu.M.Marusik, 6.i.2011
25755	*Mocyta*	sp. 4 cf. *M. clientula* sensu Benick	f	ISRAEL, Judean Hills, 1 km E Beit Shemesh, 31°44'N 35°00'E, 230m, [IL-12] Yu.M.Marusik, 6.i.2011

Table 18 (cont.)

sample	genus	species	sex	label
25756	*Mocyta*	sp. 3	m	ISRAEL, Judean Hills, 1 km E Beit Shemesh, 31°44'N 35°00'E, 230m, [IL-12] Yu.M.Marusik, 6.i.2011
25757	*Mocyta*	sp. 3	f	ISRAEL, Judean Hills, 1 km E Beit Shemesh, 31°44'N 35°00'E, 230m, [IL-12] Yu.M.Marusik, 6.i.2011
25758	*Mocyta*	sp. 3	f	TURKEY, Bursa Prov., Inkaya Area, Uludağ Nat Park, 40°09'55"N 29°01'E, 622m, pine litter, [T-23], Yu.M.Marusik 24.ix.2010
25759	*Mocyta*	sp. 3	m	TURKEY, Bursa Prov., Inkaya Area, Uludağ Nat Park, 40°09'55"N 29°01'E, 622m, pine litter, [T-23], Yu.M.Marusik 24.ix.2010
25760	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	RUSSIA, 15 km S Tomsk, 56°19'N 84°40'E, birch forest, in leaf litter, A. Babenko 20.v.2011
25761	*Mocyta*	*orbata* (Erichson, 1837)	m	TAJIKISTAN, S slope of Gissarskiy Mt. Range, 5.5 km SE Angisht Pass, 38°55.546'N 68°27.858'E, ±3m, 3069m, under stones and in grass near water source, in litter, [TjN8(058)] S.Saluk 8-12.viii.2011
25762	*Mocyta*	*amblystegii* (Brundin, 1952)	m	RUSSIA, N part of Kamchatka Peninsula, Penzhyna River, env. of Kamenskoye Village, 62.454°N 166.191°E, tall grass (Poaceae) meadow by creek, between *Salix* patch and vegetable garden, A.S. Ryabukhin 9.vii.2011
25763	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	RUSSIA, N part of Kamchatka Peninsula, Penzhyna River, env. of Kamenskoye Village, 62.454°N 166.191°E, tall grass (Poaceae) meadow by creek, between *Salix* patch and vegetable garden, A.S. Ryabukhin 9.vii.2011
25764	*Acrotona*	*parens* (Mulsant & Rey, 1852)	m	ITALY, Lombardia, Mantua, 6 km NW Mantua, Riservo Naturale Bosco Fontana, 45º11.972'N 10º44.787'E WGS84, accuracy 3m, extent 5m, h=0m, meadows in forest, in hay pile [4947] [Garmin 60CSx] V.I.Gusarov 3.vi.2011
25765	*Acrotona*	*parens* (Mulsant & Rey, 1852)	f	ITALY, Lombardia, Mantua, 6 km NW Mantua, Riservo Naturale Bosco Fontana, 45º11.972'N 10º44.787'E WGS84, accuracy 3m, extent 5m, h=0m, meadows in forest, in hay pile [4947] [Garmin 60CSx] V.I.Gusarov 3.vi.2011
25766	*Mocyta*	cf. *vagepunctata* (Wollaston, 1862)	m	SPAIN, Canary Islands, Gran Canaria, Hwy GC-600, 6 km SW Vega de San Mateo, 27º58.097'N 15º33.954'W ±7m, extent 20m, h=1877m, pine (Pinus canariensis) forest and bushes (Fabaceae), in ant nest under stones [4277] [Garmin 60CSx; WGS84] V.I.Gusarov 6.i.2010
25767	*Mocyta*	cf. *vagepunctata* (Wollaston, 1862)	f	SPAIN, Canary Islands, Gran Canaria, Hwy GC-600, 6 km SW Vega de San Mateo, 27º58.097'N 15º33.954'W ±7m, extent 20m, h=1877m, pine (*Pinus canariensis*) forest and bushes (*Fabaceae*), in ant nest under stones [4277] [Garmin 60CSx; WGS84] V.I.Gusarov 6.i.2010
25768	*Mocyta*	sp. 6	m	GEORGIA, Adjara, Batumi, Batumi Botanical Garden, 41°41'44.7"N 41°42'44.3"E, 30 m, sifting litter, [13] Marusik Y.M. 21.vii.2012

Table 18 (cont.)

sample	genus	species	sex	label
25769	*Mocyta*	sp. 6	f	GEORGIA, Adjara, Batumi, Batumi Botanical Garden, 41°41'44.7"N 41°42'44.3"E, 30 m, sifting litter, [13] Marusik Y.M. 21.vii.2012
25770	*Mocyta*	sp. 7	f	GEORGIA, Adjara, Batumi, Batumi Botanical Garden, 41°41'44.7"N 41°42'44.3"E, 30 m, sifting litter, [13] Marusik Y.M. 21.vii.2012
25771	*Mocyta*	*orbata* (Erichson, 1837)	m	GEORGIA, Kura River upper reaches, gorge, 41°37'22.3"N 43°03'39.0"E, 887 m, litter [18], Marusik Y.M. 22.vii.2012
25772	*Mocyta*	*orbata* (Erichson, 1837)	f	GEORGIA, Kura River upper reaches, gorge, 41°37'22.3"N 43°03'39.0"E, 887 m, litter [18], Marusik Y.M. 22.vii.2012
25773	*Mocyta*	*scopula* (Casey, 1893)	m	CANADA, Ontario, Hald.-Nor. Co., St. Williams Backus Tract, A.Brunke 4.x.2010
25774	*Mocyta*	*scopula* (Casey, 1893)	f	CANADA, Ontario, Hald.-Nor. Co., St. Williams Backus Tract, A.Brunke 4.x.2010
25775	*Mocyta*	*breviuscula* (Mäklin, 1852)	m	CANADA, Ontario, Lake Huron, Manitoulin Is., Kip Fleming Tract, litter, S.Paiero 29.ix.2010
25776	*Mocyta*	*breviuscula* (Mäklin, 1852)	f	CANADA, Ontario, Lake Huron, Manitoulin Is., Kip Fleming Tract, litter, S.Paiero 29.ix.2010
25777	*Mocyta*	sp. 2 near *amblystegii*	m	CANADA, Ontario, Lake Huron, Manitoulin Is., Kip Fleming Tract, litter, S.Paiero 29.ix.2010
25778	*Mocyta*	sp. 2 near *amblystegii*	f	CANADA, Ontario, Lake Huron, Manitoulin Is., Kip Fleming Tract, litter, S.Paiero 29.ix.2010
25779	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	SWITZERLAND, canton de Genève, 1.5 km N Dardagny, Route des Baillets, 46º12.406'N 5º59.730'E WGS84, accuracy 7m, extent 1 km, h=404m [Garmin 60CSx] A.Gontarenko 11.v.2013
25780	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	SWITZERLAND, canton de Genève, 1.5 km N Dardagny, Route des Baillets, 46º12.406'N 5º59.730'E WGS84, accuracy 7m, extent 1 km, h=404m [Garmin 60CSx] A.Gontarenko 11.v.2013
25781	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	RUSSIA, Irkutsk Reg., Katangskiy Distr., Podvoloshino, Nizhnyaya Tunguska River Valley, A.Shavrin & I.Enustschenko 4-9.viii.2008
25782	*Mocyta*	*laticollis* (Stephens, 1832)	f	RUSSIA, SE Krasnoyarsk Reg., Aban, Aban River, 56°40.342'N 96°05.648'E, 820', A.V.Shavrin 19.vi.2009
25783	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	RUSSIA, Chita Reg., Uletovskiy Distr., Sokhondinskiy Nature Reserve, stream without name (right tributary of Ingoda River), 2 km NE Ashagley winter cabin, 54°367'N 111°07'952", 1350m, A.V.Shavrin & I.V.Enustchenko 20.vii.2009
25784	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	U.K., Essex, Chelmsford, 51.7°N 0.5°E, P.M.Hammond 29.v.2012
25785	*Mocyta*	sp. 7	m	U.K., London, Acton Park, 53.06°N 2.98°W, P.M.Hammond 13.xi.2012
25786	*Mocyta*	sp. 7	f	U.K., London, Acton Park, 53.06°N 2.98°W, P.M.Hammond 13.xi.2012

Table 18 (cont.)

sample	genus	species	sex	label
25787	*Mocyta*	sp. 7	m	U.K., London, Acton Park, 53.06°N 2.98°W, P.M.Hammond 13.xi.2012
25788	*Mocyta*	*amplicollis* (Mulsant & Rey, 1874)	m	U.K., Devon, Ottery St Mary, SY0996, 50.75°N 3.28°W, flood refuse, P.M.Hammond 2012
25789	*Mocyta*	*fungi* (Gravenhorst, 1806)	f	U.K., Devon, Ottery St Mary, SY0996, 50.75°N 3.28°W, flood refuse, P.M.Hammond 2012
25790	*Mocyta*	sp. 3	f	TURKEY, Antalya Prov., Alanya Distr., slopes of Alanya Castle (Damlataş side), 36°32'11.6"N 31°59'30.3"E, h=50m, pine forest, litter and under stones, in shaded and open places, [A10a], Yu.M.Marusik 7.i.2013
25872	*Mocyta*	sp. 6	m	TURKEY, Antalya Prov., Alanya Distr., environs of Kestel Town, Dim valley, 36°32'34.5"N 32°06'17.5"E, h=110m, pine with oak forest, sifting & under stones, [A03], Yu.M.Marusik 2-9.i.2013
25873	*Mocyta*	sp. 6	f	TURKEY, Antalya Prov., Alanya Distr., environs of Kestel Town, Dim valley, 36°32'34.5"N 32°06'17.5"E, h=110m, pine with oak forest, sifting & under stones, [A03], Yu.M.Marusik 2-9.i.2013
25874	*Mocyta*	sp. 3	f	UKRAINE, Crimea, Yalta env., Cape Martian Nat. Res., 44°30’36.3”N 34°15’6.9”E, h=85 m, mediterranean forest, sifting leaf litter [CR-12-30, 162], N.N. Yunakov 28.iv.2012
25875	*Mocyta*	sp. 3	m	UKRAINE, Crimea, Simferopol Distr., Kessler's forest [Kesslersky Les], 44°54'32.6”N 34°11'37.8”E [Garmin eTrex; WGS84], accuracy 6m, h=431m, mixed nemoral forest, sifting leaf litter [CR-10-72, 086] N.Yunakov 10.vi.2010
25876	*Mocyta*	sp. 3	f	UKRAINE, Crimea, Simferopol Distr., Kessler's forest [Kesslersky Les], 44°54'32.6”N 34°11'37.8”E [Garmin eTrex; WGS84], accuracy 6m, h=431m, mixed nemoral forest, sifting leaf litter [CR-10-72, 086] N.Yunakov 10.vi.2010
25877	*Mocyta*	sp. 3	f	UKRAINE, Crimea, Simferopol Distr., Kessler's forest [Kesslersky Les], 44°54'32.6”N 34°11'37.8”E [Garmin eTrex; WGS84], accuracy 6m, h=431m, mixed nemoral forest, sifting leaf litter [CR-10-72, 086] N.Yunakov 10.vi.2010
25878	*Mocyta*	sp. 7	m	RUSSIA, Krasnodar Terr., Adler distr., env. of Kepsha, 43º38.393’N 40º04.716’E WGS84, accuracy 5m, extent 9m, h=266m, left bank of the Kepsha river, wet meadow nr. river, *Carex*, *Equisetum majus*, *Lamium* [C-87] [Garmin 60CSx] V.I.Gusarov 17.ix.2013

Appendix 2: Primers

Table 19: Overview of primers, amplification strategies and annealing temperatures (Ta) used in this study.

Gene	Primer	Dir.	Sequence (5'-3')	Reference	Amplification strategies	Ta C°
CO1	LCO1490	F	GGT CAA CAA ATC ATA AAG ATA TTG G	Folmer et al. 1994	LCO1490 + C1-2416ra	49
	C1-2416ra	R	GGA ATT AAA ATT TTT AGA TGA TTA GC	Elven et al. 2010		
	TY-J-1460	F	TAC AAT TTA TCG CCT AAA CTT CAG CC	Simon et al. 1994	TY-J-1460 + C1-N-2416m-r	50
	TY-J-1461	F	CAA TTT ACC GCC TAA CTC AGC CA	Modification of TY-J-1460	TY-J-1461 + C1-N-2416m-r	50
	C1-N-2416m-r	R	GGA ATC AAA ATT TTT AGT TGA TTA GC	Modification of C1-2416ra		
CO1	C1-J-2183	F	CAA CAT TTA TTT TGA TTT TTT GG	Simon et al. 1994	C1-2183 + C1-N-2416m-r	50
	C1-1730	F	TGA CTT GTW CCA TTA ATA TTA GG	New	C1-1730 + C1-N-2416m-r	50
	C1-1730m	F	TGA CTT GTA CCC TTA ATA TTA GG	Modification of C1-1730m	C1-1730m + C1-N-2416m-r	50
NADH2 to CO1	N2-1020m	F	TTT TTA GGA TTT TTC CCA AAA TG	New	N2-1020m + C1-1562m3r	50
	N2-732m3	F	CAT TTT TGA TTC CCT GAA GTA ATA GAA GGA	Modification of N2-N-732 from Simon et al. 1994	N2-1020m + C1-1562m2r	50
	N2-732m4	F	GCC CCC TTT CAT TTT TGA TTC CCT GAA GT	Modification of N2-N-732 from Simon et al. 1994	N2-732m3 + C1-1562m3r	50
	C1-1562m3r	R	GAAGTTCCTACTATTCCTGCTCA	New	N2-732m3 + C1-1562m2r	50
	C1-1562m2r	R	GAAGTTCCTACTATTCC	New	N2-732m4 + C1-1562m3r	50
					N2-732m4 + C1-1562m2r	50
ITS1	CAS18sF1	F	TACACACCGCCCGTCGCTACTA	Ji et al. 2003	CAS18sF1 + CAS5p8sB1d	67
	CAS5p8sB1d	R	ATGTGCGTTCTAAATGTCGATGTTCA	Ji et al. 2003		
ITS2	CAS5p8sFc	F	TGAACATCGACATTTYGAACGCACAT	Ji et al. 2003	CAS5p8sFc + CAS28sB1d	62
	CAS28sB1d	R	TTCTTTTCCTCCSCTTAYTRATATGCTTAA	Ji et al. 2003		

Appendix 3: Model tests

Table 20: Details for the models selected by *jModeltest* 2 for ITS2 (AIC to the left and BIC to the right).

ITS2, AIC - Model selected			
Model	TVM+I		
partition	12314		
-lnL	2183.5012		
K	228		
freqA	0.2440	**R(a)**	0.6245
freqC	0.2168	**R(b)**	3.4418
freqG	0.2538	**R(c)**	2.7808
freqT	0.2855	**R(d)**	0.2197
ti/tv	-	**R(e)**	3.4418
		R(f)	1.0000
p-inv	0.6640	**gamma**	-

ITS2, BIC - Model selected			
Model	TVMef+I		
partition	12314		
-lnL	2187.7819		
K	225		
freqA	-	**R(a)**	0.5073
freqC	-	**R(b)**	3.1104
freqG	-	**R(c)**	2.7009
freqT	-	**R(d)**	0.1837
ti/tv	-	**R(e)**	3.1104
		R(f)	1.0000
p-inv	0.6630	**gamma**	-

Table 21: Details for the model selected by *jModeltest 2* for the CO1 alignment (same for AIC and BIC).

CO1, AIC and BIC - Model selected			
Model	TIM2+I+G		
partition	010232		
-lnL	5164.1480		
K	232		
freqA	0.3294	**R(a)**	13.9177
freqC	0.1434	**R(b)**	52.0794
freqG	0.1325	**R(c)**	13.9177
freqT	0.3948	**R(d)**	1.0000
ti/tv	-	**R(e)**	107.4364
		R(f)	1.0000
p-inv	0.5770	**gamma**	0.8330

Appendix 4: Species Delimitation

Table 22: The average K2P-distances between groups in the CO1 and ITS2 clade datasets are listed in the column marked 'Distance' under the respective header ('CO1' and 'ITS2') and the columns marked 'Std. Err.' shows the standard error of the respective distances. 'Group 1' and 'Group 2' shows the groups compared. Distances that are equal to or larger than the 10X threshold, 0.1986 for CO1 and 0.0470 and for ITS2, are marked with bold types.

		CO1		ITS2	
Group 1	**Group 2**	**Distance**	**Std. Err.**	**Distance**	**Std. Err.**
25755 IL	25745 GR	0.1378	0.0154	**0.0782**	0.0109
Clade A	25745 GR	0.1046	0.0129	0.0249	0.0061
Clade A	25755 IL	0.1718	0.0173	**0.0642**	0.0101
Clade A	Clade B	0.1126	0.0132	0.0099	0.0035
Clade A	Clade C	0.1536	0.0162	**0.0483**	0.0083
Clade A	Clade D	0.1510	0.0166	0.0281	0.0060
Clade A	Clade E	0.1768	0.0179	**0.0747**	0.0107
Clade A	Clade F	0.1910	0.0180	**0.1091**	0.0128
Clade A	Clade G	0.1434	0.0143	0.0382	0.0071
Clade A	Outgroup 1	**0.2224**	0.0207	-	-
Clade A	Outgroup 2	**0.2337**	0.0219	**-**	-
Clade B	25745 GR	0.0629	0.0095	0.0179	0.0050
Clade B	25755 IL	0.1281	0.0143	**0.0634**	0.0100
Clade B	Clade C	0.1124	0.0123	0.0461	0.0081
Clade B	Clade D	0.1045	0.0121	0.0228	0.0056
Clade B	Clade E	0.1307	0.0139	**0.0727**	0.0107
Clade B	Clade F	0.1401	0.0132	**0.1081**	0.0129
Clade B	Clade G	0.1178	0.0118	0.0339	0.0068
Clade B	Outgroup 1	**0.1988**	0.0205	-	-
Clade B	Outgroup 2	**0.2302**	0.0227	**-**	-
Clade C	25745 GR	0.1244	0.0138	**0.0570**	0.0088
Clade C	25755 IL	0.1372	0.0147	**0.0710**	0.0100
Clade C	Clade D	0.0918	0.0111	0.0392	0.0076
Clade C	Clade E	0.1243	0.0130	**0.0786**	0.0108
Clade C	Clade F	0.1418	0.0135	**0.1171**	0.0132
Clade C	Clade G	0.1174	0.0120	**0.0582**	0.0088
Clade C	Outgroup 1	0.1835	0.0184	**-**	-
Clade C	Outgroup 2	**0.2069**	0.0199	**-**	-
Clade D	25745 GR	0.1114	0.0135	0.0416	0.0076
Clade D	25755 IL	0.1245	0.0153	**0.0656**	0.0098
Clade D	Clade E	0.1266	0.0149	**0.0713**	0.0104
Clade D	Clade F	0.1272	0.0136	**0.1091**	0.0126
Clade D	Clade G	0.0949	0.0113	0.0365	0.0074
Clade D	Outgroup 1	0.1803	0.0187	**-**	-
Clade D	Outgroup 2	**0.2191**	0.0231	**-**	-
Clade E	25745 GR	0.1316	0.0141	**0.0824**	0.0113
Clade E	25755 IL	0.0784	0.0108	0.0256	0.0062
Clade E	Clade F	0.1018	0.0108	**0.1022**	0.0125
Clade E	Clade G	0.1202	0.0125	**0.0786**	0.0114
Clade E	Outgroup 1	0.1834	0.0196	**-**	-
Clade E	Outgroup 2	**0.2212**	0.0220	-	-
Clade F	25745 GR	0.1486	0.0146	0.1208	0.0140
Clade F	25755 IL	0.0966	0.0112	0.0968	0.0124

Table 22 (cont.)

		CO1		ITS2	
Group 1	**Group 2**	**Distance**	**Std. Err.**	**Distance**	**Std. Err.**
Clade F	Clade G	0.1358	0.0133	0.1107	0.0129
Clade F	Outgroup 1	0.1975	0.0194	-	-
Clade F	Outgroup 2	**0.2134**	0.0199	-	-
Clade G	25745 GR	0.1117	0.0119	0.0514	0.0084
Clade G	25755 IL	0.1262	0.0135	0.0710	0.0108
Clade G	Outgroup 1	0.1808	0.0180	-	-
Clade G	Outgroup 2	0.1860	0.0191	-	-
Outgroup 1	25745 GR	**0.2008**	0.0201	-	-
Outgroup 1	25755 IL	0.1577	0.0177	-	-
Outgroup 1	Outgroup 2	0.1809	0.0186	-	-
Outgroup 2	25745 GR	**0.2365**	0.0236	-	-
Outgroup 2	25755 IL	**0.2000**	0.0210	-	-

Table 23: The average K2P-distances between groups in the CO1 and ITS2 morphospecies datasets are listed in the column marked 'Distance' under the respective header ('CO1' and 'ITS2') and the columns marked 'Std. Err.' shows the standard error of the respective distances. 'Group 1' and 'Group 2' shows the groups compared. Distances that are equal to or larger than the 10X threshold, 0.1986 for CO1 and 0.0470 and for ITS2, are marked with bold types.

		CO1		ITS2	
Group 1	**Group 2**	**Distance**	**Std. Err.**	**Distance**	**Std. Err.**
A. muscorum	*A. silvicola*	**0.1809**	0.0187	-	-
A. muscorum	*M. amblystegii*	**0.1993**	0.0207	-	-
A. muscorum	*M. amplicollis*	**0.2055**	0.0217	-	-
A. muscorum	*M. breviuscula*	**0.2022**	0.0190	-	-
A. muscorum	*M. cf. vagepunctata*	**0.1988**	0.0201	-	-
A. muscorum	*M. fungi*	**0.2231**	0.0205	-	-
A. muscorum	*M. orbata*	**0.1834**	0.0191	-	-
A. muscorum	*Mocyta sp.2*	**0.1837**	0.0186	-	-
A. muscorum	*Mocyta sp.3*	**0.1803**	0.0187	-	-
A. muscorum	*Mocyta sp.4*	**0.1577**	0.0174	-	-
A. muscorum	*Mocyta sp.5*	**0.2008**	0.0199	-	-
A. muscorum	*Mocyta sp.6*	**0.1808**	0.0175	-	-
A. muscorum	*Mocyta sp.7*	**0.1835**	0.0180	-	-
A. silvicola	*M. amblystegii*	**0.2158**	0.0220	-	-
A. silvicola	*M. amplicollis*	**0.2020**	0.0198	-	-
A. silvicola	*M. breviuscula*	**0.2118**	0.0202	-	-
A. silvicola	*M. cf. vagepunctata*	**0.2302**	0.0225	-	-
A. silvicola	*M. fungi*	**0.2345**	0.0221	-	-
A. silvicola	*M. orbata*	**0.2212**	0.0214	-	-
A. silvicola	*Mocyta sp.2*	**0.2281**	0.0222	-	-
A. silvicola	*Mocyta sp.3*	**0.2191**	0.0230	-	-
A. silvicola	*Mocyta sp.4*	**0.2000**	0.0204	-	-
A. silvicola	*Mocyta sp.5*	**0.2365**	0.0233	-	-
A. silvicola	*Mocyta sp.6*	**0.1860**	0.0191	-	-
A. silvicola	*Mocyta sp.7*	**0.2069**	0.0198	-	-

Table 23 (cont.)

		CO1		ITS2	
Group 1	**Group 2**	**Distance**	**Std. Err.**	**Distance**	**Std. Err.**
M. amblystegii	*M. amplicollis*	0.0453	0.0081	0.0178	0.0046
M. amblystegii	*M. breviuscula*	**0.1720**	0.0174	**0.1098**	0.0132
M. amblystegii	*M. cf. vagepunctata*	0.1468	0.0156	**0.1077**	0.0135
M. amblystegii	*M. fungi*	**0.1915**	0.0191	**0.1096**	0.0138
M. amblystegii	*M. orbata*	0.1037	0.0130	**0.1007**	0.0126
M. amblystegii	*Mocyta sp.2*	0.0664	0.0096	0.0239	0.0057
M. amblystegii	*Mocyta sp.3*	0.1224	0.0145	**0.1094**	0.0134
M. amblystegii	*Mocyta sp.4*	0.0992	0.0132	**0.0935**	0.0121
M. amblystegii	*Mocyta sp.5*	0.1475	0.0164	**0.1200**	0.0146
M. amblystegii	*Mocyta sp.6*	0.1333	0.0140	**0.1125**	0.0133
M. amblystegii	*Mocyta sp.7*	0.1414	0.0145	**0.1145**	0.0135
M. amplicollis	*M. breviuscula*	**0.1832**	0.0180	**0.1223**	0.0145
M. amplicollis	*M. cf. vagepunctata*	0.1476	0.0150	**0.1211**	0.0148
M. amplicollis	*M. fungi*	**0.2027**	0.0195	**0.1218**	0.0150
M. amplicollis	*M. orbata*	0.0993	0.0116	**0.1144**	0.0139
M. amplicollis	*Mocyta sp.2*	0.0777	0.0105	0.0359	0.0074
M. amplicollis	*Mocyta sp.3*	0.1325	0.0147	**0.1226**	0.0147
M. amplicollis	*Mocyta sp.4*	0.1016	0.0131	**0.1107**	0.0139
M. amplicollis	*Mocyta sp.5*	**0.1532**	0.0160	**0.1334**	0.0159
M. amplicollis	*Mocyta sp.6*	0.1370	0.0140	**0.1222**	0.0144
M. amplicollis	*Mocyta sp.7*	0.1443	0.0145	**0.1313**	0.0150
M. breviuscula	*M. cf. vagepunctata*	0.1053	0.0122	0.0121	0.0040
M. breviuscula	*M. fungi*	0.0533	0.0078	0.0106	0.0037
M. breviuscula	*M. orbata*	**0.1720**	0.0175	**0.0771**	0.0104
M. breviuscula	*Mocyta sp.2*	**0.1630**	0.0161	**0.0918**	0.0120
M. breviuscula	*Mocyta sp.3*	0.1286	0.0142	0.0286	0.0062
M. breviuscula	*Mocyta sp.4*	**0.1581**	0.0159	**0.0695**	0.0103
M. breviuscula	*Mocyta sp.5*	0.1048	0.0127	0.0305	0.0067
M. breviuscula	*Mocyta sp.6*	0.1282	0.0129	**0.0425**	0.0074
M. breviuscula	*Mocyta sp.7*	0.1332	0.0140	**0.0478**	0.0080
M. cf. vagepunctata	*M. fungi*	0.1129	0.0129	0.0098	0.0038
M. cf. vagepunctata	*M. orbata*	0.1307	0.0135	**0.0727**	0.0105
M. cf. vagepunctata	*Mocyta sp.2*	0.1220	0.0132	**0.0889**	0.0121
M. cf. vagepunctata	*Mocyta sp.3*	0.1045	0.0122	0.0228	0.0058
M. cf. vagepunctata	*Mocyta sp.4*	0.1281	0.0140	**0.0634**	0.0099
M. cf. vagepunctata	*Mocyta sp.5*	0.0629	0.0093	0.0179	0.0052
M. cf. vagepunctata	*Mocyta sp.6*	0.1178	0.0113	0.0339	0.0068
M. cf. vagepunctata	*Mocyta sp.7*	0.1124	0.0122	**0.0424**	0.0075
M. fungi	*M. orbata*	**0.1770**	0.0176	**0.0747**	0.0107
M. fungi	*Mocyta sp.2*	**0.1752**	0.0168	**0.0896**	0.0123
M. fungi	*Mocyta sp.3*	**0.1518**	0.0164	0.0281	0.0064
M. fungi	*Mocyta sp.4*	**0.1723**	0.0170	**0.0640**	0.0099
M. fungi	*Mocyta sp.5*	0.1046	0.0128	0.0247	0.0063

Table 23 (cont.)

		CO1		ITS2	
Group 1	**Group 2**	**Distance**	**Std. Err.**	**Distance**	**Std. Err.**
M. fungi	*Mocyta sp.6*	0.1440	0.0142	0.0380	0.0071
M. fungi	*Mocyta sp.7*	**0.1543**	0.0162	**0.0434**	0.0076
M. orbata	*Mocyta sp.2*	0.1038	0.0125	**0.0854**	0.0118
M. orbata	*Mocyta sp.3*	0.1266	0.0147	**0.0713**	0.0103
M. orbata	*Mocyta sp.4*	0.0784	0.0107	0.0256	0.0059
M. orbata	*Mocyta sp.5*	0.1316	0.0140	**0.0824**	0.0116
M. orbata	*Mocyta sp.6*	0.1202	0.0123	**0.0786**	0.0112
M. orbata	*Mocyta sp.7*	0.1243	0.0129	**0.0782**	0.0105
Mocyta sp.2	*Mocyta sp.3*	0.1240	0.0145	**0.0885**	0.0121
Mocyta sp.2	*Mocyta sp.4*	0.0866	0.0115	**0.0793**	0.0115
Mocyta sp.2	*Mocyta sp.5*	0.1428	0.0156	**0.1029**	0.0131
Mocyta sp.2	*Mocyta sp.6*	0.1365	0.0143	**0.0917**	0.0120
Mocyta sp.2	*Mocyta sp.7*	0.1384	0.0139	**0.0954**	0.0120
Mocyta sp.3	*Mocyta sp.4*	0.1245	0.0152	**0.0656**	0.0099
Mocyta sp.3	*Mocyta sp.5*	0.1114	0.0135	**0.0416**	0.0081
Mocyta sp.3	*Mocyta sp.6*	0.0949	0.0110	0.0365	0.0075
Mocyta sp.3	*Mocyta sp.7*	0.0918	0.0107	0.0381	0.0073
Mocyta sp.4	*Mocyta sp.5*	0.1378	0.0153	**0.0782**	0.0111
Mocyta sp.4	*Mocyta sp.6*	0.1262	0.0134	**0.0710**	0.0106
Mocyta sp.4	*Mocyta sp.7*	0.1372	0.0143	**0.0702**	0.0097
Mocyta sp.5	*Mocyta sp.6*	0.1117	0.0117	**0.0514**	0.0087
Mocyta sp.5	*Mocyta sp.7*	0.1244	0.0136	**0.0537**	0.0086
Mocyta sp.6	*Mocyta sp.7*	0.1174	0.0117	**0.0561**	0.0087

Table 24: The average K2P-distances between groups in the CO1 SMC dataset are listed in the column marked 'Distance' and the column marked 'Std. Err.' shows the standard error of the respective distances. 'Group 1' and 'Group 2' shows the groups compared. Distances that are equal to or larger than the 10X threshold (0.0986) are marked with bold types.

Group 1	Group 2	Distance	Std. Err.
A. muscorum	*A. silvicola*	**0.1809**	0.0187
A. muscorum	*M. amblystegii*	**0.1993**	0.0206
A. muscorum	*M. amplicollis*	**0.2055**	0.0218
A. muscorum	*M. breviuscula*	**0.2022**	0.0193
A. muscorum	*M. cf. vagepunctata*	**0.1988**	0.0199
A. muscorum	*M. fungi 1*	**0.2232**	0.0208
A. muscorum	*M. fungi 2*	**0.2222**	0.0216
A. muscorum	*M. orbata*	**0.1834**	0.0192
A. muscorum	*Mocyta sp.2*	**0.1837**	0.0184
A. muscorum	*Mocyta sp.3*	**0.1803**	0.0185
A. muscorum	*Mocyta sp.4*	**0.1577**	0.0177
A. muscorum	*Mocyta sp.5*	**0.2008**	0.0204
A. muscorum	*Mocyta sp.6 1*	**0.1707**	0.0177

Table 24 (cont.)

Group 1	Group 2	Distance	Std. Err.
A. muscorum	*Mocyta sp.6 2*	**0.1868**	0.0188
A. muscorum	*Mocyta sp.7 1*	**0.1874**	0.0183
A. muscorum	*Mocyta sp.7 2*	**0.1818**	0.0187
A. silvicola	*M. amblystegii*	**0.2158**	0.0223
A. silvicola	*M. amplicollis*	**0.2020**	0.0200
A. silvicola	*M. breviuscula*	**0.2118**	0.0207
A. silvicola	*M. cf. vagepunctata*	**0.2302**	0.0234
A. silvicola	*M. fungi 1*	**0.2351**	0.0226
A. silvicola	*M. fungi 2*	**0.2236**	0.0219
A. silvicola	*M. orbata*	**0.2212**	0.0223
A. silvicola	*Mocyta sp.2*	**0.2281**	0.0222
A. silvicola	*Mocyta sp.3*	**0.2191**	0.0235
A. silvicola	*Mocyta sp.4*	**0.2000**	0.0206
A. silvicola	*Mocyta sp.5*	**0.2365**	0.0241
A. silvicola	*Mocyta sp.6 1*	**0.1853**	0.0206
A. silvicola	*Mocyta sp.6 2*	**0.1864**	0.0199
A. silvicola	*Mocyta sp.7 1*	**0.2089**	0.0207
A. silvicola	*Mocyta sp.7 2*	**0.2060**	0.0207
M. amblystegii	*M. amplicollis*	0.0453	0.0082
M. amblystegii	*M. breviuscula*	**0.1720**	0.0178
M. amblystegii	*M. cf. vagepunctata*	**0.1468**	0.0154
M. amblystegii	*M. fungi 1*	**0.1922**	0.0197
M. amblystegii	*M. fungi 2*	**0.1796**	0.0190
M. amblystegii	*M. orbata*	**0.1037**	0.0129
M. amblystegii	*Mocyta sp.2*	0.0664	0.0094
M. amblystegii	*Mocyta sp.3*	**0.1224**	0.0145
M. amblystegii	*Mocyta sp.4*	**0.0992**	0.0129
M. amblystegii	*Mocyta sp.5*	**0.1475**	0.0162
M. amblystegii	*Mocyta sp.6 1*	**0.1318**	0.0147
M. amblystegii	*Mocyta sp.6 2*	**0.1342**	0.0149
M. amblystegii	*Mocyta sp.7 1*	**0.1431**	0.0148
M. amblystegii	*Mocyta sp.7 2*	**0.1406**	0.0154
M. amplicollis	*M. breviuscula*	**0.1832**	0.0184
M. amplicollis	*M. cf. vagepunctata*	**0.1476**	0.0151
M. amplicollis	*M. fungi 1*	**0.2035**	0.0202
M. amplicollis	*M. fungi 2*	**0.1897**	0.0193
M. amplicollis	*M. orbata*	**0.0993**	0.0115
M. amplicollis	*Mocyta sp.2*	0.0777	0.0105
M. amplicollis	*Mocyta sp.3*	**0.1325**	0.0150
M. amplicollis	*Mocyta sp.4*	**0.1016**	0.0131
M. amplicollis	*Mocyta sp.5*	**0.1532**	0.0157
M. amplicollis	*Mocyta sp.6 1*	**0.1410**	0.0154
M. amplicollis	*Mocyta sp.6 2*	**0.1346**	0.0145
M. amplicollis	*Mocyta sp.7 1*	**0.1514**	0.0154

Table 24 (cont.)

Group 1	Group 2	Distance	Std. Err.
M. amplicollis	*Mocyta sp.7 2*	**0.1413**	0.0148
M. breviuscula	*M. cf. vagepunctata*	**0.1053**	0.0121
M. breviuscula	*M. fungi 1*	0.0534	0.0079
M. breviuscula	*M. fungi 2*	0.0505	0.0076
M. breviuscula	*M. orbata*	**0.1720**	0.0180
M. breviuscula	*Mocyta sp.2*	**0.1630**	0.0164
M. breviuscula	*Mocyta sp.3*	**0.1286**	0.0142
M. breviuscula	*Mocyta sp.4*	**0.1581**	0.0162
M. breviuscula	*Mocyta sp.5*	**0.1048**	0.0129
M. breviuscula	*Mocyta sp.6 1*	**0.1262**	0.0144
M. breviuscula	*Mocyta sp.6 2*	**0.1293**	0.0134
M. breviuscula	*Mocyta sp.7 1*	**0.1351**	0.0143
M. breviuscula	*Mocyta sp.7 2*	**0.1323**	0.0147
M. cf. vagepunctata	*M. fungi 1*	**0.1132**	0.0132
M. cf. vagepunctata	*M. fungi 2*	**0.1074**	0.0129
M. cf. vagepunctata	*M. orbata*	**0.1307**	0.0138
M. cf. vagepunctata	*Mocyta sp.2*	**0.1220**	0.0133
M. cf. vagepunctata	*Mocyta sp.3*	**0.1045**	0.0119
M. cf. vagepunctata	*Mocyta sp.4*	**0.1281**	0.0142
M. cf. vagepunctata	*Mocyta sp.5*	0.0629	0.0093
M. cf. vagepunctata	*Mocyta sp.6 1*	**0.1204**	0.0130
M. cf. vagepunctata	*Mocyta sp.6 2*	**0.1163**	0.0121
M. cf. vagepunctata	*Mocyta sp.7 1*	**0.1139**	0.0127
M. cf. vagepunctata	*Mocyta sp.7 2*	**0.1118**	0.0125
M. fungi 1	*M. orbata*	**0.1774**	0.0185
M. fungi 1	*Mocyta sp.2*	**0.1757**	0.0175
M. fungi 1	*Mocyta sp.3*	**0.1522**	0.0166
M. fungi 1	*Mocyta sp.4*	**0.1727**	0.0178
M. fungi 1	*Mocyta sp.5*	**0.1052**	0.0132
M. fungi 1	*Mocyta sp.6 1*	**0.1359**	0.0151
M. fungi 1	*Mocyta sp.6 2*	**0.1499**	0.0151
M. fungi 1	*Mocyta sp.7 1*	**0.1546**	0.0164
M. fungi 1	*Mocyta sp.7 2*	**0.1547**	0.0171
M. fungi 2	*M. fungi 1*	0.0390	0.0064
M. fungi 2	*M. orbata*	**0.1701**	0.0180
M. fungi 2	*Mocyta sp.2*	**0.1655**	0.0168
M. fungi 2	*Mocyta sp.3*	**0.1438**	0.0162
M. fungi 2	*Mocyta sp.4*	**0.1650**	0.0176
M. fungi 2	*Mocyta sp.5*	0.0946	0.0117
M. fungi 2	*Mocyta sp.6 1*	**0.1287**	0.0146
M. fungi 2	*Mocyta sp.6 2*	**0.1331**	0.0141
M. fungi 2	*Mocyta sp.7 1*	**0.1486**	0.0161
M. fungi 2	*Mocyta sp.7 2*	**0.1491**	0.0168
M. orbata	*Mocyta sp.2*	**0.1038**	0.0124

Table 24 (cont.)

Group 1	Group 2	Distance	Std. Err.
M. orbata	*Mocyta sp.3*	**0.1266**	0.0149
M. orbata	*Mocyta sp.4*	0.0784	0.0109
M. orbata	*Mocyta sp.5*	**0.1316**	0.0143
M. orbata	*Mocyta sp.6 1*	**0.1194**	0.0135
M. orbata	*Mocyta sp.6 2*	**0.1206**	0.0132
M. orbata	*Mocyta sp.7 1*	**0.1288**	0.0137
M. orbata	*Mocyta sp.7 2*	**0.1224**	0.0133
Mocyta sp.2	*Mocyta sp.3*	**0.1240**	0.0147
Mocyta sp.2	*Mocyta sp.4*	0.0866	0.0114
Mocyta sp.2	*Mocyta sp.5*	**0.1428**	0.0154
Mocyta sp.2	*Mocyta sp.6 1*	**0.1376**	0.0153
Mocyta sp.2	*Mocyta sp.6 2*	**0.1359**	0.0152
Mocyta sp.2	*Mocyta sp.7 1*	**0.1442**	0.0147
Mocyta sp.2	*Mocyta sp.7 2*	**0.1358**	0.0144
Mocyta sp.3	*Mocyta sp.4*	**0.1245**	0.0152
Mocyta sp.3	*Mocyta sp.5*	**0.1114**	0.0133
Mocyta sp.3	*Mocyta sp.6 1*	0.0889	0.0119
Mocyta sp.3	*Mocyta sp.6 2*	0.0985	0.0122
Mocyta sp.3	*Mocyta sp.7 1*	0.0885	0.0103
Mocyta sp.3	*Mocyta sp.7 2*	0.0932	0.0114
Mocyta sp.4	*Mocyta sp.5*	**0.1378**	0.0154
Mocyta sp.4	*Mocyta sp.6 1*	**0.1233**	0.0141
Mocyta sp.4	*Mocyta sp.6 2*	**0.1279**	0.0144
Mocyta sp.4	*Mocyta sp.7 1*	**0.1409**	0.0150
Mocyta sp.4	*Mocyta sp.7 2*	**0.1356**	0.0147
Mocyta sp.5	*Mocyta sp.6 1*	**0.1103**	0.0128
Mocyta sp.5	*Mocyta sp.6 2*	**0.1126**	0.0122
Mocyta sp.5	*Mocyta sp.7 1*	**0.1253**	0.0140
Mocyta sp.5	*Mocyta sp.7 2*	**0.1240**	0.0142
Mocyta sp.6 1	*Mocyta sp.7 1*	**0.1045**	0.0119
Mocyta sp.6 1	*Mocyta sp.7 2*	**0.1120**	0.0132
Mocyta sp.6 2	*Mocyta sp.6 1*	0.0577	0.0079
Mocyta sp.6 2	*Mocyta sp.7 1*	**0.1180**	0.0127
Mocyta sp.6 2	*Mocyta sp.7 2*	**0.1237**	0.0136
Mocyta sp.7 1	*Mocyta sp.7 2*	0.0390	0.0060

Table 25: The average K2P-distances between groups in the ITS SMC dataset are listed in the column marked 'Distance' and the column marked 'Std. Err.' shows the standard error of the respective distances. 'Group 1' and 'Group 2' shows the groups compared. Distances that are equal to or larger than the 10X threshold (0.0052) are marked with bold types.

Group 1	Group 2	Distance	Std. Err.
M. amblystegii 1	*M. amblystegii 2*	**0.0145**	0.0045
M. amblystegii 1	*M. amplicollis*	**0.0101**	0.0040
M. amblystegii 2	*M. amplicollis*	**0.0255**	0.0061
M. amblystegii 1	*M. breviuscula*	**0.1105**	0.0135
M. amblystegii 2	*M. breviuscula*	**0.1091**	0.0131
M. amplicollis	*M. breviuscula*	**0.1223**	0.0145
M. amblystegii 1	*M. cf. vagepunctata*	**0.1094**	0.0136
M. amblystegii 2	*M. cf. vagepunctata*	**0.1061**	0.0132
M. amplicollis	*M. cf. vagepunctata*	**0.1211**	0.0147
M. breviuscula	*M. cf. vagepunctata*	**0.0121**	0.0039
M. amblystegii 1	*M. fungi 7*	**0.1121**	0.0139
M. amblystegii 2	*M. fungi 7*	**0.1070**	0.0134
M. amplicollis	*M. fungi 7*	**0.1218**	0.0148
M. breviuscula	*M. fungi 7*	**0.0106**	0.0036
M. cf. vagepunctata	*M. fungi 7*	**0.0098**	0.0036
M. amblystegii 1	*M. orbata*	**0.1042**	0.0129
M. amblystegii 2	*M. orbata*	**0.0972**	0.0127
M. amplicollis	*M. orbata*	**0.1144**	0.0139
M. breviuscula	*M. orbata*	**0.0771**	0.0104
M. cf. vagepunctata	*M. orbata*	**0.0727**	0.0104
M. fungi 7	*M. orbata*	**0.0747**	0.0104
M. amblystegii 1	*Mocyta sp. 2*	**0.0264**	0.0062
M. amblystegii 2	*Mocyta sp. 2*	**0.0214**	0.0059
M. amplicollis	*Mocyta sp. 2*	**0.0359**	0.0076
M. breviuscula	*Mocyta sp. 2*	**0.0918**	0.0120
M. cf. vagepunctata	*Mocyta sp. 2*	**0.0889**	0.0121
M. fungi 7	*Mocyta sp. 2*	**0.0896**	0.0122
M. orbata	*Mocyta sp. 2*	**0.0854**	0.0120
M. amblystegii 1	*Mocyta sp. 3*	**0.1112**	0.0134
M. amblystegii 2	*Mocyta sp. 3*	**0.1076**	0.0128
M. amplicollis	*Mocyta sp. 3*	**0.1226**	0.0143
M. breviuscula	*Mocyta sp. 3*	**0.0286**	0.0061
M. cf. vagepunctata	*Mocyta sp. 3*	**0.0228**	0.0056
M. fungi 7	*Mocyta sp. 3*	**0.0281**	0.0063
M. orbata	*Mocyta sp. 3*	**0.0713**	0.0101
Mocyta sp. 2	*Mocyta sp. 3*	**0.0885**	0.0118
M. amblystegii 1	*Mocyta sp. 4*	**0.0979**	0.0127
M. amblystegii 2	*Mocyta sp. 4*	**0.0890**	0.0123
M. amplicollis	*Mocyta sp. 4*	**0.1107**	0.0140
M. breviuscula	*Mocyta sp. 4*	**0.0695**	0.0104
M. cf. vagepunctata	*Mocyta sp. 4*	**0.0634**	0.0100
M. fungi 7	*Mocyta sp. 4*	**0.0640**	0.0099
M. orbata	*Mocyta sp. 4*	**0.0256**	0.0063
Mocyta sp. 2	*Mocyta sp. 4*	**0.0793**	0.0119
Mocyta sp. 3	*Mocyta sp. 4*	**0.0656**	0.0098
M. amblystegii 1	*Mocyta sp. 5*	**0.1216**	0.0149
M. amblystegii 2	*Mocyta sp. 5*	**0.1184**	0.0144
M. amplicollis	*Mocyta sp. 5*	**0.1334**	0.0160
M. breviuscula	*Mocyta sp. 5*	**0.0305**	0.0064

Table 25 (cont.)

Group 1	Group 2	Distance	Std. Err.
M. cf. vagepunctata	*Mocyta sp. 5*	**0.0179**	0.0050
M. fungi 7	*Mocyta sp. 5*	**0.0247**	0.0061
M. orbata	*Mocyta sp. 5*	**0.0824**	0.0113
Mocyta sp. 2	*Mocyta sp. 5*	**0.1029**	0.0132
Mocyta sp. 3	*Mocyta sp. 5*	**0.0416**	0.0076
Mocyta sp. 4	*Mocyta sp. 5*	**0.0782**	0.0110
M. amblystegii 1	*Mocyta sp. 6 3*	**0.1129**	0.0137
M. amblystegii 2	*Mocyta sp. 6 3*	**0.1097**	0.0134
M. amplicollis	*Mocyta sp. 6 3*	**0.1209**	0.0147
M. breviuscula	*Mocyta sp. 6 3*	**0.0415**	0.0077
M. cf. vagepunctata	*Mocyta sp. 6 3*	**0.0323**	0.0070
M. fungi 7	*Mocyta sp. 6 3*	**0.0377**	0.0075
M. orbata	*Mocyta sp. 6 3*	**0.0763**	0.0111
Mocyta sp. 2	*Mocyta sp. 6 3*	**0.0905**	0.0121
Mocyta sp. 3	*Mocyta sp. 6 3*	**0.0340**	0.0073
Mocyta sp. 4	*Mocyta sp. 6 3*	**0.0687**	0.0106
Mocyta sp. 5	*Mocyta sp. 6 3*	**0.0497**	0.0086
M. amblystegii 1	*Mocyta sp. 6 1*	**0.1133**	0.0134
M. amblystegii 2	*Mocyta sp. 6 1*	**0.1101**	0.0131
M. amplicollis	*Mocyta sp. 6 1*	**0.1213**	0.0143
M. breviuscula	*Mocyta sp. 6 1*	**0.0438**	0.0077
M. cf. vagepunctata	*Mocyta sp. 6 1*	**0.0362**	0.0074
M. fungi 7	*Mocyta sp. 6 1*	**0.0382**	0.0074
M. orbata	*Mocyta sp. 6 1*	**0.0785**	0.0112
Mocyta sp. 2	*Mocyta sp. 6 1*	**0.0909**	0.0118
Mocyta sp. 3	*Mocyta sp. 6 1*	**0.0379**	0.0077
Mocyta sp. 4	*Mocyta sp. 6 1*	**0.0709**	0.0107
Mocyta sp. 5	*Mocyta sp. 6 1*	**0.0537**	0.0089
Mocyta sp. 6 3	*Mocyta sp. 6 1*	**0.0059**	0.0029
M. amblystegii 1	*Mocyta sp. 6 2*	**0.1172**	0.0140
M. amblystegii 2	*Mocyta sp. 6 2*	**0.1139**	0.0137
M. amplicollis	*Mocyta sp. 6 2*	**0.1254**	0.0149
M. breviuscula	*Mocyta sp. 6 2*	**0.0421**	0.0078
M. cf. vagepunctata	*Mocyta sp. 6 2*	**0.0328**	0.0070
M. fungi 7	*Mocyta sp. 6 2*	**0.0382**	0.0077
M. orbata	*Mocyta sp. 6 2*	**0.0822**	0.0117
Mocyta sp. 2	*Mocyta sp. 6 2*	**0.0947**	0.0125
Mocyta sp. 3	*Mocyta sp. 6 2*	**0.0379**	0.0078
Mocyta sp. 4	*Mocyta sp. 6 2*	**0.0745**	0.0112
Mocyta sp. 5	*Mocyta sp. 6 2*	**0.0503**	0.0085
Mocyta sp. 6 3	*Mocyta sp. 6 2*	**0.0059**	0.0026
Mocyta sp. 6 1	*Mocyta sp. 6 2*	**0.0064**	0.0031
M. amblystegii 1	*Mocyta sp. 7 2*	**0.1168**	0.0138
M. amblystegii 2	*Mocyta sp. 7 2*	**0.1131**	0.0135
M. amplicollis	*Mocyta sp. 7 2*	**0.1319**	0.0151
M. breviuscula	*Mocyta sp. 7 2*	**0.0507**	0.0088
M. cf. vagepunctata	*Mocyta sp. 7 2*	**0.0447**	0.0084
M. fungi 7	*Mocyta sp. 7 2*	**0.0468**	0.0086
M. orbata	*Mocyta sp. 7 2*	**0.0835**	0.0113
Mocyta sp. 2	*Mocyta sp. 7 2*	**0.0959**	0.0122
Mocyta sp. 3	*Mocyta sp. 7 2*	**0.0394**	0.0080
Mocyta sp. 4	*Mocyta sp. 7 2*	**0.0743**	0.0104
Mocyta sp. 5	*Mocyta sp. 7 2*	**0.0556**	0.0092
Mocyta sp. 6 3	*Mocyta sp. 7 2*	**0.0582**	0.0092

Table 25 (cont.)

Group 1	Group 2	Distance	Std. Err.
Mocyta sp. 6 1	*Mocyta sp. 7 2*	**0.0570**	0.0091
Mocyta sp. 6 2	*Mocyta sp. 7 2*	**0.0606**	0.0096
M. amblystegii 1	*Mocyta sp. 7 1*	**0.1176**	0.0136
M. amblystegii 2	*Mocyta sp. 7 1*	**0.1139**	0.0134
M. amplicollis	*Mocyta sp. 7 1*	**0.1331**	0.0151
M. breviuscula	*Mocyta sp. 7 1*	**0.0498**	0.0088
M. cf. vagepunctata	*Mocyta sp. 7 1*	**0.0439**	0.0085
M. fungi 7	*Mocyta sp. 7 1*	**0.0460**	0.0087
M. orbata	*Mocyta sp. 7 1*	**0.0827**	0.0111
Mocyta sp. 2	*Mocyta sp. 7 1*	**0.0967**	0.0121
Mocyta sp. 3	*Mocyta sp. 7 1*	**0.0386**	0.0081
Mocyta sp. 4	*Mocyta sp. 7 1*	**0.0735**	0.0103
Mocyta sp. 5	*Mocyta sp. 7 1*	**0.0548**	0.0093
Mocyta sp. 6 3	*Mocyta sp. 7 1*	**0.0574**	0.0091
Mocyta sp. 6 1	*Mocyta sp. 7 1*	**0.0562**	0.0091
Mocyta sp. 6 2	*Mocyta sp. 7 1*	**0.0597**	0.0095
Mocyta sp. 7 2	*Mocyta sp. 7 1*	**0.0072**	0.0033
M. amblystegii 1	*Mocyta sp. 7 3*	**0.1168**	0.0137
M. amblystegii 2	*Mocyta sp. 7 3*	**0.1131**	0.0134
M. amplicollis	*Mocyta sp. 7 3*	**0.1326**	0.0150
M. breviuscula	*Mocyta sp. 7 3*	**0.0541**	0.0091
M. cf. vagepunctata	*Mocyta sp. 7 3*	**0.0481**	0.0087
M. fungi 7	*Mocyta sp. 7 3*	**0.0503**	0.0090
M. orbata	*Mocyta sp. 7 3*	**0.0729**	0.0106
Mocyta sp. 2	*Mocyta sp. 7 3*	**0.0959**	0.0121
Mocyta sp. 3	*Mocyta sp. 7 3*	**0.0394**	0.0079
Mocyta sp. 4	*Mocyta sp. 7 3*	**0.0673**	0.0098
Mocyta sp. 5	*Mocyta sp. 7 3*	**0.0591**	0.0094
Mocyta sp. 6 3	*Mocyta sp. 7 3*	**0.0582**	0.0091
Mocyta sp. 6 1	*Mocyta sp. 7 3*	**0.0570**	0.0090
Mocyta sp. 6 2	*Mocyta sp. 7 3*	**0.0606**	0.0095
Mocyta sp. 7 2	*Mocyta sp. 7 3*	**0.0096**	0.0038
Mocyta sp. 7 1	*Mocyta sp. 7 3*	**0.0104**	0.0037

Appendix 5: Haplotypes

Table 26: Overview of the CO1 and ITS2 haplotypes assigned to each specimen, sorted by sample number.

Sample	Species	Country	Haplotype	
			CO1	ITS2
308	*Mocyta amblystegii*	RUSSIA	63	26
595	*Mocyta fungi*	BELARUS	10	6
599	*Mocyta fungi*	BELARUS	9	6
857	*Mocyta fungi*	U.K.	1	1
905	*Mocyta orbata*	UKRAINE	59	22
5042	*Mocyta breviuscula*	U.S.A.	34	12
5681	*Mocyta sp. 6*	GREECE	67	29
5957	*Mocyta orbata*	RUSSIA	54	23
7544	*Mocyta fungi*	SLOVAKIA	26	1
7611	*Mocyta orbata*	GREECE	51	22
7645	*Mocyta sp. 3*	GREECE	46	21
7691	*Mocyta orbata*	GREECE	51	22
7726	*Mocyta orbata*	GREECE	52	22
8006	*Mocyta fungi*	GREECE	8	8
9108	*Mocyta fungi*	LITHUANIA	7	1
9174	*Mocyta amblystegii*	RUSSIA	62	27
10517	*Mocyta orbata*	TURKEY	57	22
11227	*Mocyta fungi*	NORWAY	1	1
11237	*Mocyta fungi*	NORWAY	16	1
11260	*Mocyta fungi*	NORWAY	29	1
11261	*Mocyta fungi*	NORWAY	5	7
11730	*Mocyta orbata*	TAJIKISTAN	51	22
12109	*Mocyta fungi*	RUSSIA	22	3
13657	*Mocyta fungi*	NORWAY	5	1
13661	*Mocyta fungi*	NORWAY	15	1
17358	*Mocyta fungi*	RUSSIA	14	1
17359	*Mocyta fungi*	LITHUANIA	1	1
17360	*Mocyta fungi*	U.S.A.	24	10
17361	*Mocyta fungi*	U.S.A.	1	1
17450	*Mocyta orbata*	GEORGIA	56	22
17452	*Mocyta orbata*	GEORGIA	51	22
22350	*Mocyta fungi*	FRANCE	3	9
23175	*Mocyta fungi*	SWITZERLAND	3	1
24370	*Mocyta fungi*	NORWAY	19	1
24387	*Mocyta fungi*	NORWAY	21	1
24453	*Mocyta fungi*	NORWAY	32	1
24460	*Mocyta fungi*	NORWAY	31	1
24461	*Mocyta amplicollis*	NORWAY	61	25
24462	*Mocyta fungi*	NORWAY	13	1
24464	*Mocyta fungi*	NORWAY	2	1
24466	*Mocyta fungi*	NORWAY	1	1
24467	*Mocyta fungi*	NORWAY	2	1
24468	*Mocyta fungi*	NORWAY	2	1
24469	*Mocyta fungi*	NORWAY	2	1
24470	*Mocyta fungi*	NORWAY	4	1
24471	*Mocyta fungi*	NORWAY	27	1
24472	*Mocyta fungi*	NORWAY	2	1

Table 26 (cont.)

Sample	Species	Country	Haplotype	
			CO1	ITS2
24473	*Mocyta fungi*	NORWAY	25	1
24474	*Mocyta fungi*	NORWAY	2	1
24475	*Mocyta fungi*	NORWAY	2	1
24476	*Mocyta fungi*	NORWAY	4	4
24479	*Mocyta fungi*	NORWAY	18	11
24480	*Mocyta fungi*	NORWAY	1	1
24481	*Mocyta fungi*	NORWAY	12	1
24482	*Mocyta fungi*	NORWAY	2	1
24483	*Mocyta fungi*	FRANCE	3	1
24643	*Mocyta sp. 3*	UKRAINE	45	21
24990	*Mocyta sp. 6*	RUSSIA	68	31
25728	*Mocyta sp. 7*	UKRAINE	40	18
25729	*Mocyta orbata*	UKRAINE	51	22
25730	*Mocyta orbata*	UKRAINE	53	22
25731	*Mocyta orbata*	UKRAINE	51	24
25732	*Mocyta orbata*	UKRAINE	58	22
25733	*Mocyta fungi*	BELARUS	6	2
25734	*Mocyta fungi*	RUSSIA	4	5
25735	*Mocyta fungi*	RUSSIA	4	1
25736	*Mocyta fungi*	NORWAY	23	1
25737	*Mocyta fungi*	NORWAY	20	1
25738	*Mocyta fungi*	NORWAY	33	1
25739	*Mocyta amplicollis*	U.K.	60	25
25740	*Mocyta fungi*	U.K.	30	1
25741	*Mocyta cf. vagepunctata*	SPAIN	37	14
25743	*Mocyta sp. 6*	GREECE	67	32
25744	*Mocyta sp. 6*	GREECE	67	33
25745	*Mocyta sp. 5*	GREECE	36	15
25746	*Mocyta fungi*	U.S.A.	1	1
25749	*Mocyta fungi*	U.S.A.	1	1
25750	*Mocyta sp. 7*	FRANCE	42	17
25751	*Mocyta sp. 7*	FRANCE	41	17
25752	*Mocyta sp. 7*	FRANCE	40	17
25753	*Mocyta sp. 7*	FRANCE	40	17
25755	*Mocyta sp. 4 cf. M. clientula sensu* Benick	ISRAEL	66	28
25758	*Mocyta sp. 3*	TURKEY	50	21
25759	*Mocyta sp. 3*	TURKEY	46	21
25760	*Mocyta fungi*	RUSSIA	17	1
25761	*Mocyta orbata*	TAJIKISTAN	51	22
25767	*Mocyta cf. vagepunctata*	SPAIN	38	14
25768	*Mocyta sp. 6*	GEORGIA	70	31
25769	*Mocyta sp. 6*	GEORGIA	69	31
25770	*Mocyta sp. 7*	GEORGIA	44	16
25771	*Mocyta orbata*	GEORGIA	55	22
25772	*Mocyta orbata*	GEORGIA	52	22
25775	*Mocyta breviuscula*	CANADA	35	13
25777	*Mocyta sp. 2*	CANADA	65	20
25778	*Mocyta sp. 2*	CANADA	64	20
25779	*Mocyta fungi*	SWITZERLAND	28	1
25780	*Mocyta fungi*	SWITZERLAND	3	1
25784	*Mocyta fungi*	U.K.	11	1

Table 26 (cont.)

Sample	Species	Country	Haplotype	
			CO1	ITS2
25785	*Mocyta sp. 7*	U.K.	39	18
25786	*Mocyta sp. 7*	U.K.	39	18
25787	*Mocyta sp. 7*	U.K.	39	1
25788	*Mocyta amplicollis*	U.K.	60	25
25789	*Mocyta fungi*	U.K.	1	1
25790	*Mocyta sp. 3*	TURKEY	49	21
25872	*Mocyta sp. 6*	TURKEY	72	30
25873	*Mocyta sp. 6*	TURKEY	71	30
25874	*Mocyta sp. 3*	UKRAINE	45	21
25875	*Mocyta sp. 3*	UKRAINE	45	21
25876	*Mocyta sp. 3*	UKRAINE	47	21
25877	*Mocyta sp. 3*	UKRAINE	48	21
25878	*Mocyta sp. 7*	RUSSIA	43	19

Appendix 6: Data Management

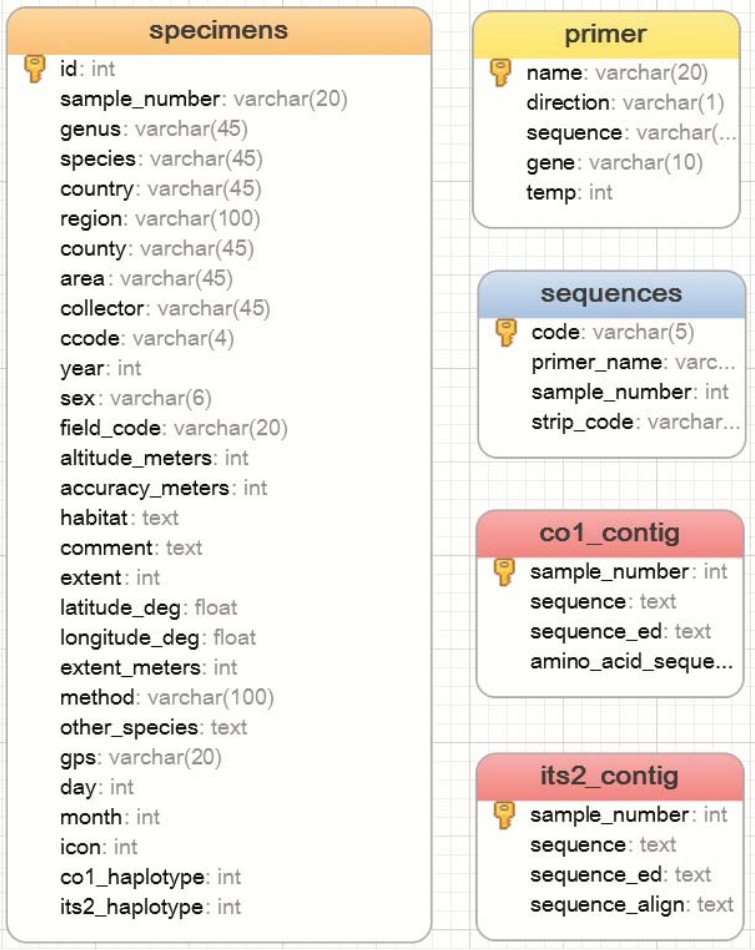

Figure 17: Illustration of the MySQL database layout, containing five tables: 'specimens' contains all label information in addition to haplotype numbers for both CO1 and ITS2; 'primers' contains all information for the primers used; 'sequences' contains the codes used for the samples delivered to StarSeq with linkage to sample number; 'co1_contig' and 'its2_contig' contains the sequences for the respective markers, both raw and aligned sequences. Screen dump from *Navicat for MySQL*.

```
var mysql      = require('mysql');
var fs = require('fs');

var connection = mysql.createConnection({
  host     : 'eilen2.mysql.domeneshop.no',
  user     : [redacted]
  password : [redacted]
  database : 'eilen2'
});

////////////////////////////////////// CO1 ////////////////////////////////////
//////////////////////////// CO1 aligned Fasta-file ///////////////////////////
connection.connect();

var filename = "CO1_aligned.fas";
if(process.argv.length > 2) {
filename = process.argv[2];
}
connection.query(
 'SELECT *, b.sequence co1, c.sequence its2 '
 + 'FROM  specimens a, co1_contig b, its2_contig c '
 + 'WHERE a.sample_number = b.sample_number '
 + 'AND a.sample_number = c.sample_number '
 + 'AND b.sequence IS NOT NULL '
 + 'AND  c.sequence IS NOT NULL', function(err, rows, fields) {
  if (err) throw err;
  var stream = fs.createWriteStream(filename);

    stream.once('open', function(fd) {
        for(var i = 0;i<rows.length;i++) {
            var row = rows[i];
            var lineone = row.sample_number;
            if(row.ccode){lineone = lineone + row.ccode}
            if(row.co1) {
                stream.write('>' + lineone + "\n")
                stream.write(row.co1 + "\n");
            }
        }
        stream.end();
        console.log("all data written");
    });
});
connection.end();
```

Figure 18: node script for making FASTA file containing aligned CO1 sequences for all samples which also have ITS2 sequences available. For making other FASTA files the 'connection.query' was edited.

Appendix 7: ML Trees

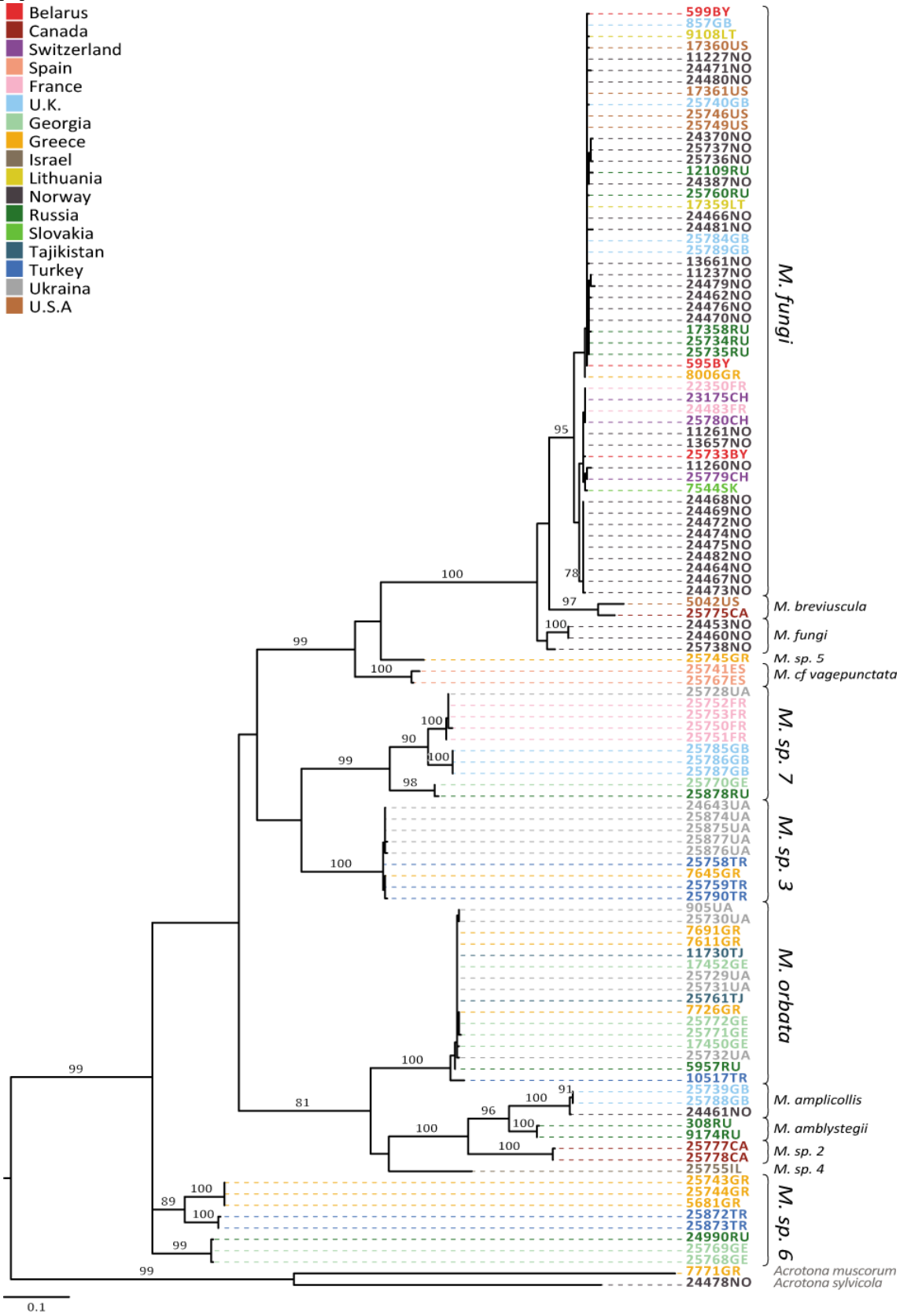

Figure 19: Tree from the Maximum likelihood analyses of CO1 (TIM2+I+G). Bootstrap values listed above branches, values below 75 were removed. Scale bar indicate substitutions per site.

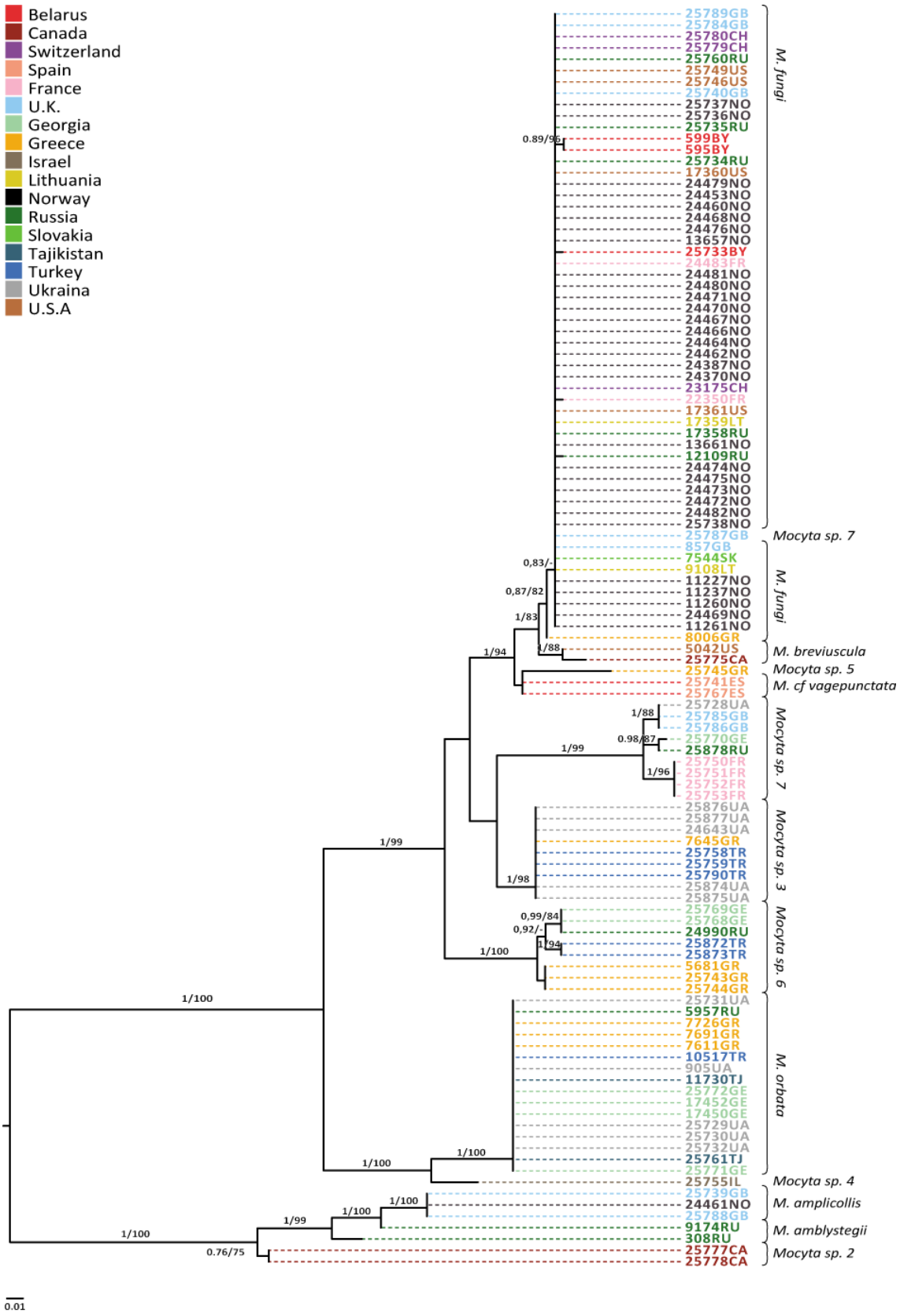

Figure 20: Tree from the Maximum likelihood analyses of ITS2 (TVMef+I). Bootstrap values listed above branches, values below 75 were removed. Scale bar indicate substitutions per site.